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57 TFLLYTVANTYIPHLPPPLVYLAWPVYWFCQSCILTGLWVLGHECGHHAFSEYQWIDNAV 116
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hes 322; Conservative
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Matches
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116, Appl
117, Appl
118, Appl
119, Appl
119, Appl
111, A
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1 MSDSYDDRMKDHDMDERAPI.....IYIEQDADSKHKGTYWYHKM 378
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Sequence 41
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l: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
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GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
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US-09-059-769-4
US-09-161-994A-2
US-09-059-769-12
US-09-059-769-12
US-09-059-769-11
US-09-161-994A-15
US-09-161-994A-15
US-09-161-994A-15
US-09-837-751-31
US-09-161-994A-14
US-09-161-914-914
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Maximum Match 100%
Listing first 45 summaries
                                                                                                         - protein search, using sw model
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Maximum DB seq length: 200000000
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APPLICANT: Hitz, William D
TITLE OF INVENTION: Fatty Acid Modifying Enzymes From
TITLE OF INVENTION: Developing Seeds of Vernonia galamenensis
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,302
                                       US-09-354-231B-14
US-09-133-962A-4
US-09-128-602B-10
US-09-925-297-10
US-09-995-297-14
US-09-697-379-4
US-09-697-379-4
US-09-771-904A-10
US-09-771-904A-10
US-09-771-904A-10
US-09-371-904A-10
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US-09-995-297-12
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STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
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CLASSIFICATION: 435
ATTORNEY/AGENT INPORMATION:
NAME: Majarian, William R
REGISTRATION NUMBER: P-41,173
REPRENCE/POCKET NUMBER: BB-1084
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEPRAX: 302-773-0164
                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08872302
Patent No. 5846784
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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amino acid
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MOLECULE TYPE: protein
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4,

Length 384; Indels

87.3%; Score 1821; DB 1; 84.3%; Pred. No. 1.6e-179; iive 29; Mismatches 27;

67

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246 ACMYGVPVLGVFTFFDVITFLHHTHQSSPHYDSTEWNWIRGALSAIDRDFGFLNSVFHDV 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 MCMYGVPVIGLNSFIIVITYLHHTHLSSPHYDSTEWNWIKGALTTIDRDFGLLNRVFHDV
                                                                                                                                                                                                                                                                       8 RMKDHDMDERAPIDPAPFSLSDLKKAIPAHCFRRSAVWSSCYVVQDLIITFLLYTVANTY
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Patent No. 6329518
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Singh, Surinder
APPLICANT: Styne, Sten
TITLE OF INVENTION: Plant Patty Acid Epoxygenase Genes and UNIBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
                                                                                                                                                Length 374;
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MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elem PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059,769
FILING DATE: B-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PO6223
FILING DATE: 15-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PO6226
FILING DATE: 15-APR-1997
PRIOR APPLICATION DATA:
APPLICATION D
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                                                                                                                                                72.4%; Score 1510; DB 2; 70.4%; Pred. No. 2.1e-147; tive 50; Mismatches 56;
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                                                                                                                                                      Query Match
Best Local Similarity 70.4<sup>1</sup>
Matches 261; Conservative
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                                                     MOLECULE TYPE: protein US-09-059-769-4
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      amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 FGLLNRVFHDVTHTHVLHHLFPYIPHYHAKEASDAIKPVLGEYRMIDRTPFYKAMWREAK 362
GFVLHSALLTPYFSWKYSHRKHHANTNSLENEEVYIPRTQSQLRTYSTYEFLDNTPGRIL 176
                                                                                                                                                                                                                  177 ILVIMLTLGFPLYLLTNVSGKKYDRFTNHFDPLSPIFTERERIQVALSDLGIVAVFYGLK 236
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APPLICANT: Singh, Surinder
APPLICANT: Singh, Surinder
APPLICANT: Singh, Surinder
APPLICANT: Lenman, Marit
APPLICANT: Lenman, Marit
APPLICANT: Stymne, Sten
APPLICANT: Stymne, Sten
APPLICANT: Stymne, Sten
APPLICANT: Stymne, Sten
APPLICANT: Stymner and Sullivan, P.C.
STREET: S170 Manhattan Circle, Suite 201
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CAPPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
CORPATER: PER PC COMPATISH
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059,769
FILING DATE: April 14, 1998
PRIOR APPLICATION NUMBER: US/09/0523
FILING DATE: 15-APR-1997
PRIOR APPLICATION NUMBER: US 60/043706
FILING DATE: 15-APR-1997
PRIOR APPLICATION NUMBER: US 60/043706
FILING DATE: 16-APR-1997
PRIOR APPLICATION NUMBER: US 60/050403
FILING DATE: 10-APR-1997
PRIOR APPLICATION NUMBER: US 60/050403
FILING DATE: 10-DATA:
APPLICATION NUMBER: US 60/050403
FILING DATE: 20-JUN-1997
ATTORIEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ECIYIEQDADSKHKGTYWYHKM 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ECIYIEPDEDKKHKGVYWYHKM 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09059769; Patent No. 6329518; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION: (303) 499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPAX: (303) 499-8089
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids
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STATE: Colorad
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US-09-059-769-4
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SEQ ID NO 2
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TITLE OF INVENTION: NOVEL PLANT ENZYME AND USE THEREOF
FILE REFERENCE: BAFOR=1
                                                                                                                                                                                                                                                                                             Query Match 71.6%; Score 1493; DB 2; Best Local Similarity 70.1%; Pred. No. 1.2e-145; Matches 260; Conservative 47; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PILE REPERENCE: BAFOR=1
CURRENT APPLICATION NUMBER: US/09/161,994A
CURRENT PILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 9601236.4
PRIOR FILING DATE: 1996-03-29
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver: 2.0
                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/050403
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09161994A
Patent No. 6333448
                                                                          NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REPERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8089
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DAHLOVIST, Anders
GUMMESON, Per-Clov
LEE, Michael
SJODAL, Staffan
STYMNE, Sten
                                                                                                                                                                       TYPE: amino acids TOPOLOGY: 1:-
   16-APR-1997
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BANAS, Antoni
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APPLICANT: BAFOR,
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US-09-161-994A-2
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APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT: Cahoon, Edgar B
APPLICANT: Hitz, William D
APPLICANT: Ripp, Kevin G
TITLE OF INVENTION: FATTY ACID CONTAINING DELTA-8,10,12 CONUGATED DOUBLE
TITLE OF INVENTION: FOUNDS
TITLE OF INVENTION: BONDS
TITLE OF INVENTION: BONDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/638,937
CURRENT FILING DATE: 1999-08-16
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Microsoft Office 97
SEQ ID NO 15
LENGTH: 383
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                                                                                                                                                                                8 RMKDHDMDERAPIDPAPFSLSDLKKAIPAHCFRRSAVWSSCYVVQDLIITFLLYTVANTY
                                                                                                                                                                                                                                                                                                                                                                     128 YFSWKYSHRKHHANTNSLENEEVYIPRTOSOLRTYSTYEFLDNTPGRILILVIMLTLGFP
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                                                                                         Length 375;
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                                                                                                                                       Indels
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                                                                                           DB 2;
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60.1%; Pred. No. 1.6e-123;
                                                                                         68.4%; Score 1427.5; DB 2
65.9%; Pred. No. 7.1e-139;
cive 56; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62; Mismatches
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; Sequence 15, Application US/09638937
; Patent No. 6593514
; GENERAL INFORMATION:
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                                                                                         Query Match
Best Local Similarity 65.9%
Matches 244; Conservative
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Best Local Similarity 60.1'
Matches 218; Conservative
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TYPE: PRT
CRGANISM: Crepis alpina
US-09-161-994A-2
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Gaps

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76 VYLAMPVYMPCQSCILTGLWVLGHECGHHAFSEYQMIDNAVGFVLHSALLTPYFSWKYSH 135
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                                                                                                                                                Length 383;
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APPLICANT: BAFOR, Maureen
APPLICANT: BAFOR, Maureen
APPLICANT: BAROS, Antoni
APPLICANT: BALOS, Antoni
APPLICANT: GUMMESON, Per-Olov
APPLICANT: LEE, Machael
APPLICANT: LEE, Machael
APPLICANT: STVANE, Sten
APPLICANT: STVANE, Sten
APPLICANT: STVANE, Sten
APPLICANT: STVANE, Sten
APPLICANT: LEMMAN, Maxit
APPLICANT: LEMMAN, Maxit
TITLE OF INVENTION: NOVEL: PLANT ENZYME AND USE THEREOF
FILE REFERENCE: BAFOR=1
CURRENT PILING DATE: 1998-09-29
PRIOR PLING DATE: 1998-03-29
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PARENTIN VET: 2.0
SEGUED NO 16 SEGUED NOS: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 60.9%; Score 1271; DB 2; Length 3 Best Local Similarity 58.3%; Pred. No. 1.1e-122; Matches 210; Conservative 67; Mismatches 81; Indels
                                                                                                                                           Query Match 60.9%; Score 1271; DB 2; Length 3 Best Local Similarity 58.3%; Pred. No. 1.1e-122; Matches 210; Conservative 67; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16, Application US/09161994A Patent No. 6333448
                                                                                 Solanum commersonii
                 TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Glycine max
US-09-161-994A-16
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                                                                                 , ORGANISM:
US-09-059-769-12
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                                                                                                                                                                                                                                                                                                                      79 HPLSYVAWPLYWFCQGSVLTGVWVIAHECGHHAFSDYQWLDDTVGLLLHSALLVPYFSWK 138
                                          YSHRKHHANTNSLENEEVYIPRTQSQLRTYSTYEFLDNTPGRILILVIMLTLGFPLYLLT 192
                                                                                                                            193 NVSGKKYDRFTNHPDPLSPIFTERERIQVALSDLGIVAVFYGLKFLVQTKGFGWVMCMYG
                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Green, Allan
APPLICANT: Gingh, Surinder
APPLICANT: Jenman, Marit
APPLICANT: Lenman, Marit
APPLICANT: Stymne, Sten
TITLE OF INVENTION: Plant Fatty Acid Epoxygenase Genes and Uses
TITLE OF INVENTION: Therefor
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: FLORDY disk
COMPUTER: FLORDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059,769
FILING DATE: APTIL 14, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PO6223
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PO6226
FILING DATE: 15-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/043706
FILING DATE: 16-APR-1997
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/050403
FILING DATE: 10-OWN-1997
ATTONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Greenlee, Winner and Sullivan, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : 5370 Manhattan Circle, Suite 201
Boulder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 12, Application US/09059769 ; Patent No. 6329518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (303) 499-8080
TELEPAX: (303) 499-8089
INPORMATION FOR SEQ ID NO: 12: 8EQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 383 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Colorado
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ORGANISM:
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US-09-059-769-11
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                                                              256 IGLNSFIIVITYLHHTHLSSPHYDSTEWNWIKGALTTIDRDFGLLNRVFHDVTHTHVLHH 315
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                                                                                                                                                                                                                                                                                                                        82 CYIAWPIYWICQGCVCTGIWVNAHECGHHAFSDYQWVDDTVGLILHSALLVPYFSWKYSH 141
                                                                                                                         196 GKKYDRFTWHFDPLSPIFTERERIQVALSDLGIVAVFYGLKFLVQTKGFGWVMCMYGVPV 255
                                          136 RKHHANTNSLENEEVYIPRTQSQLRTYSTYEFLDNTPGRILILVIMLTLGFPLYLLTNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11, Application US/09059769
Patent No. 6129518
GENERAL INFORMATION:
APPLICANT: Green, Allan
APPLICANT: Green, Allan
APPLICANT: Singh, Surinder
APPLICANT: Stymne, Sten
TITLE OF INVENTION: Therefor
VINDER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 09/059,769
FILING DATE: April 14, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PO6223
FILING DATE: 15-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PO6226
FILING DATE: 15-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/043706
FILING DATE: 16-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/043706
FILING DATE: 20-JUN-1997
ATFORMEY ABPLICATION NUMBER: US 60/050403
FILING DATE: 20-JUN-1997
ATFORMEY ABPLICATION:
ANAME: APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: Greenlee, Winner and Sullivan, P.C. 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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MEDIUM TYPE: Floppy
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STATE: Colorac
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                                                                                                                7 DRMKDHDMDERAPIDPAPFSLSDLKKAIPAHCFRRSAVWSSCYVVQDLIITFLLYTVANT
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                                              Gaps
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      Length 383;
                                              Indels
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Query Match 59.2%; Score 1234; DB 2; Best Local Similarity 57.0%; Pred. No. 7.2e-119; Matches 211; Conservative 68; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REPERENCE: BAFOR=1
CURRENT APPLICATION NUMBER: US/09/161,994A
CURRENT FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 9601236.4
PRIOR FILING DATE: 1996-03-29
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68; Mismatches
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Patent No. 6333448
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BANAS, Antoni
BANAS, Antoni
DAHLGVIST, Anders
GUMMESON, Per-Olov
LEE, Michael
SJODAL, Staffan
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Best Local Similarity 57.0
Matches 211; Conservative
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APPLICANT: LENMAN, Marit
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260 LVVNAFLVMITYLQHTHPSLPHYDSSEWDWRRGALSTVDRDYGILNKVFHNITDTHVAHH 319
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                                                                                                                                                                                       APPLICANT: Green, Allan
APPLICANT: Singh, Surinder
APPLICANT: Singh, Surinder
APPLICANT: Liu, Qing
TITLE OF INVENTION: Method of Modifying the Content of Cottonseed
FILE REFERENCE: 45-00
CURRENT APPLICATION NUMBER: US/09/837,751
CURRENT FILING DATE: 2001-04-18
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Petentin Ver. 2.0
SEQ ID NO 6
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APPLICANT: Hitz, William D
TITLE OF INVENTION: Fatty Acid Modifying Enzymes From
TITLE OF INVENTION: Developing Seeds of Vernonia galamenensis
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: E.I. duPont de Nemours and Co.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.8%; Score 1226; DB 2; Length 3 56.9%; Pred. No. 4.8e-118; ive 72; Mismatches 81; Indels
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CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 1007
                                                                                                                                ; Sequence 6, Application US/09837751; Patent No. 6974898; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08872302
Patent No. 5846784
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Matches 205; Conservative
367 SKHKGTYWYH 376
                    371 TESKGVFWYN 380
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COMPUTER READABLE FORM:
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ORGANISM: GOBSYPium sp.
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US-08-872-302-2
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                                                                                                                                                                                             VMCMYGVPVIGLNSFIIVITYLHHTHLSSPHYDSTEWNWIKGALTTIDRDFGLLNRVFHD 306
                                                                                                                                                                                                                                                                         VTHTHVLHHLFPYIPHYHAKEASEAIKPILGDYRMIDRTPFFKAMWREAKECIYIEQDAD 366
73 YFHLLPGPLSFRGMAIYWAVQGCILTGVWVIAHECGHHAFSDYQLLDDIVGLILHSALLV 132
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                                      PYPSWKYSHRKHHANTNSLENEEVYIPRTQSQLRTYSTYEFLDNTPGRILILVIMLTLGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Green, Allan APPLICANT: Green, Surinder APPLICANT: Singh, Surinder APPLICANT: Singh, Surinder APPLICANT: Liu, Qing but a APPLICANT: Liu, Qing the Content of Cottonseed Oil FILE REFERENCE: 45-00
CURRENT PAPLICATION NUMBER: US 60/198,124
PRIOR APPLICATION NUMBER: US 60/198,124
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 31
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Patent No. 6974898
GENERAL INFORMATION:
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Matches 211; Conservative
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Sequence 41, Application US/08320982
Patent No. 5801026
GENERAL INFORMATION:
APPLICANT: SOMERVILLE, CHRIS
APPLICANT: VAN DE LOO, FRANK
TITLE OF INVENTION: PRODUCE HYDROXYLASES TO
TITLE OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHWAN DARBY & CUSHWAN L.L.P.
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252 ICLYGVPLLIVNAFLVLITYLQHTHPSLPHYDSSEWDWLRGALATVDRDYGILNKVFHNI 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              308 THTHVLHHLFPYIPHYHAKEASEAIKPILGDYRMIDRTPFFKAMWREAKECIYIEQDADS 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 LYLLTNVSGKKYDRFTNHFDPLSPIFTERERIQVALSDLGIVAVFYGLKFLVQTKGFGWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 IPHLPPPLVYLAWPVYWFCQSCILTGLWVLGHECGHHAFSEYQWIDNAVGFVLHSALLTP
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                                                                                                                SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/314,596
FILING DATE: US-SEP-1994
CLASSIFICATION: 435
ATTONREY/AGENT INPORMATION:
NAME: KOKULIS, PAUL.
REGISTRATION NUMBER: 16,773
REPRENCE/DOCKET NUMBER: 206905/1220
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAK: 202-861-3000
TELEFRAK: 202-822-0944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 58.2%; Score 1215; DB 1; Best Local Similarity 55.6%; Pred. No. 6.6e-117; Matches 205; Conservative 70; Mismatches 92;
                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-314-596-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                   COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       368 KHKGTYWYH 376
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US-08-320-982-41
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Fatent No. 5668292
GENERAL INFORMATION:
APPLICANT: SOMERVILLE, CHRIS
APPLICANT: VAN DE LOO, FRANK
TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 SSLAWLAYWVVQGCVLTGVWVIAHECGHHAPSDYQWVDDTVGFLLHSVLLVPFFSWKYSH 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 VYLAWPVYWPCQSCILTGLWVLGHECGHHAFSEYQWIDNAVGFVLHSALLTPYFSWKYSH 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 RKHHANTNSLENEEVYIPRTQSQLRTYSTYEFLDNTPGRILILVIMLTLGFPLYLLTNVS 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 BRVPYAKPPFIISDLKKAIPPHCFQRSLIRSFSYVVYDLAVSFLLYYVAATYFHHLPNPF 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 ERAPIDPAPFSLSDLKKAIPAHCFRRSAVWSSCYVVQDLIITFLLYTVANTYIPHLPPPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
S8.7%; Score 1224.5; DB 1;
Best Local Similarity 56.6%; Pred. No. 6.9e-118;
Matches 206; Conservative 72; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: GUSHMAN DARBY & CUSHMAN L.L.P.
STREET: 1100 NEW YORK AVENUE, N.W.
STATE: D.C.
COUNTRY: 11 C.
ZIP.
                                                                                                                                                                                   CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Majarian, William R
REGISTRATION NUMBER: P-41,173
REFERENCE/DOCKET NUMBER: BB-1084
TELECHOMUNICATION INFORMATION:
TELEPHONE: 302-92-4926
TELEPHONE: 302-773-0164
                                                                                                                                                                                                                                                                                                                                             TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 382 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-08-872-302-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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US-08-314-596-41
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ADDRESSEE: PILLSBURY MADISON & SUTRO L.L.P. STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON
                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIble
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION UNDERS: US/08/819,037
FILING DATE: 19-WAR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION 1939
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/320,982
FILING DATE: 11-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/314,596
FILING DATE: 26-SEP-1994
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 383 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 55.6
Matches 205; Conservative
                                                                                   STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  368 KHKGTYWYH 376
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Sequence 41, Application US/08819037

Patent No. 6028248

GENERAL INFORMATION:

APPLICANT: SOMERVILLE, CHRIS

APPLICANT: VAN DE LOO, FRANK

TITLE OF INVENTION: USE OF PLANT PATTY ACYL HYDROXYLASES TO

TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS

NUMBER OF SEQUENCES: 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LYLLTNVSGKKYDRFTNHFDPLSPIFTERERIQVALSDLGIVAVFYGLKFLVQTKGFGWV 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TDTHVAHHLFSTMPHYNAMEATKAIKPILGDYYQFDGTPWYVAMYREAKECIYVEPDREG 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 IPHLPPPLVYLAMPVYWPCQSCILTGLWVLGHECGHHAFSEYQWIDNAVGFVLHSALLTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 RMKDHDMDERAPIDPAPFSLSDLKKAIPAHCFRRSAVWSSCYVVQDLIITFLLYTVANTY
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58.2%; Score 1215; DB 1; Length 383;

Best Local Similarity 55.6%; Pred. No. 6.6e-117;

Matches 205; Conservative 70; Mismatches 92; Indels
                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTAME: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/320,982
FILING DATE: 11-CT-1994
CLASSIFICATION: 435
FRIOR APPLICATION: A35
PRIOR APPLICATION: DATA:
APPLICATION NUMBER: US 08/314,596
FILING DATE: 26-SEP-1994
ATTORNEY AGENT INFORMATION:
NAME: KOKUJIS, PAUL N.
REGISTRATION NUMBER: 266905/1220
TELEPHONE: 202-861-3000
TELEPHONE: 202-861-3000
TELEPHONE: 202-861-3000
TELEPHONE: 202-861-3000
TELEPHONE: 202-861-3000
TELEPHONE: 303-861-3000
                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
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  U.S.A.
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    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128
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127
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                                                                                                                                                                                    68 IPHLPPPLVYLAWPVYWFCQSCILTGLWVLGHECGHHAFSEYQWIDNAVGFVLHSALLTP
                                                                                                                                                                                                                                                                          128 YFSWKYSHRKHHANTNSLENEEVYIPRTQSQLRTYSTYBFLDNTPGRILILVIMLTLGFP
                                                                                           8 RMKDHDMDERAPIDPAPFSLSDLKKAIPAHCFRRSAVWSSCYVVQDLIITFLLYTVANTY
                                             Gaps
Length 383;
                                             92; Indels
58.2%; Score 1215; DB 2;
55.6%; Pred. No. 6.6e-117;
tive 70; Mismatches 92;
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Job time : 52 secs
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GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
                      Copyright
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OM protein - protein search, using sw model

September 22, 2006, 19:34:21; Search time 198 Seconds (without alignments) 872.868 Million cell updates/sec Run on:

US-10-622-774-2 Title: Perfect score:

1 MSDSYDDRMKDHDMDERAPI.....IYIEQDADSKHKGTYWYHKM 378 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2589679 segs, 457216429 residues Searched:

2589679 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq\_8:\* Database :

geneseqp2003as:\* geneseqp2003bs:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2002s:\* geneseqp2004s:\* geneseqp2005s:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2006s:\*

# SUMMARIES

		de			SUMMERIES	
Result No.	Score	Query Match	Query Match Length DB	60	ID	Description
1	2086	100.0	378	٩	ADW68587	Adw68587 Stokesia
7	2077	99.6	378	6	AEC02369	Aec02369 Stokesia
7	1821	87.3	384	~	AAW83354	Aaw83354 Vernonia
4	1549.5	74.3	377	æ	ADR87355	Adr87355 Hydroxyla
2	1549.5	74.3	377	80	ADR87357	Adr87357 Codon opt
9	1549.5	74.3	377	80	ADR87361	Adr87361 Codon opt
7	1549.5	74.3	377	6	AEC02271	Aec02271 Stokesia
80	1549.5	74.3	377	σ	AEC02275	Aec02275 Stokesia
6	1549.5	74.3	377	0	AEC02269	Aec02269 Stokesia
10	1523.5	73.0	377	4	AAB70946	Aab70946 C. offici
11	1510	72.4	374	~	AAW79743	Aaw79743 Crepis sp
12	1504	72.1	374	80	ADR87360	Adr87360 Codon opt
13	1504	72.1	374	0	AEC02274	Aec02274 Crepis bi
14	1499	71.9	374	Φ	AEC02370	Aec02370 Crepis bi
15	1498	71.8	374	Φ	ADR87337	Adr87337 Hydroxyla
16	1498	71.8	374	σ	AEC02251	Aec02251 Crepis bi
17	1497	71.8	374	σ	AEC02368	Aec02368 Crepis pa
18	1493	71.6	374	~	AAW79742	Aaw79742 Crepis pa
19	1493	71.6	374	æ	ADR87450	Adr87450 Crepis pa
20	1482	71.0	380	80	ADR87343	Adr87343 FAD2/Hydr
21	1482	71.0	380	σ	AEC02257	Aec02257 Crepis bi
22	1458	6.69	372	σ	ADX69239	Adx69239 Delta-12
23	1458	6.69	372	6	ADX85618	Adx85618 C. palaes

69.9 372 9 ADW88814 5 68.4 375 2 AAW36793 5 68.3 375 9 ADX18010 5 68.3 375 9 ADX18010 5 68.3 375 9 ADX28516 60.1 383 4 AAY7225 3 60.5 395 8 ADX71277 8 60.3 383 9 ADC014197 8 60.3 383 9 ADC02561 8 59.6 383 9 ABC02561 5 59.6 383 9 ABC02561 4 59.2 383 4 AAR3427 5 58.6 383 2 AAX8088 5 58.6 388 8 ADX81421 5 58.7 382 2 AAX8088 5 58.6 388 8 ADX8148 5 58.8 383 2 AAX8088
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### ALIGNMENTS

ADW68587 standard; protein; 378 AA. RESULT 1 ADW68587

07-APR-2005 (first entry) ADW68587;

Stokesia laevis fatty acid epoxygenase protein.

DNA purification, transgenic plant, plant, expression, recombinant DNA, seed oil; soybean oil, linseed oil; plastic, delta 12-fatty acid epoxygenase, delta 12-epoxygenase; 

delta 12-epoxidase; enzyme; transgenic.

Stokesia laevis.

US2005022270-A1.

27-JAN-2005.

21-JUL-2003; 2003US-00622774.

21-JUL-2003; 2003US-00622774.

(HILD/) HILDEBRAND D. (HATA/) HATANAKA T. ij. Hildebrand D, Hatanaka

WPI; 2005-111979/12. N-PSDB; ADW68586.

New isolated nucleic acid molecule encoding a delta 12-fatty acid epoxygenase enzyme, useful for genetically producing industrial products including coating, composites, adhesives and plasticizers.

Claim 1; SEQ ID NO 2; 22pp; English.

The present invention relates to a nucleic acid molecule encoding a delta 12-fatty acid epoxygenase enzyme. The invention is useful for genetically producing raw materials in the manufacture of industrial products including coating, composites, adhesives and plasticizers. The present sequence is the Stokesia laevis fatty acid epoxygenase protein.

Sequence 378 AA;

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100.0%; Score 2086; DB 9;
100.0%; Pred. No. 1.3e-215;
ive 0; Mismatches 0;
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  Query Match
Best Local Similarity 100.
Matches 378; Conservative
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BAUBLITE C.
KLOEK A P.
DAVILA-APONTE J A.
HRESKO M C.
HRESKO M C.
CLAIRD M B.
ZENTELLA MILLIAMS D J.
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The invention relates to a transgenic plant containing at least one DNA construct comprising: (a) a nucleic acid encoding a polypeptide effective for catalyzing the conversion of a substrate to a C16, C18, or C20 monounsaturated fatty acid product; and (b) a regulatory element operably linked to the nucleic acid encoding the polypeptide and conferring expression in a vegetative tissue of the plant. Also described: (1) a method of making a transgenic plant; (2) an isolated nucleic acid comprising the nucleotide sequence; (3) a recombinant nucleic acid construct comprising at least one regulatory element that confers expression in a vegetative tissue of a plant; and (4) a method of expression in a vegetative tissue of a plant; and (4) a method of plant is useful in preparing compounds having anthelminic activity. The present sequence represents an epoxygenase which is used in the construction of the present invention.
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218 or C20 monounsaturated fatty acid product, useful in preparing
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                                                                                                                                                                                                                                                                                                                                                                              Length 378;
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Pred. No. 1.3e-214;
1; Mismatches 1;
                                                  Claim 21; SEQ ID NO 136; 130pp; English
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(first entry)
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376; Conservative
                anthelmintic compounds.
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10-FEB-1999
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Matches 376
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                                                                                                                                   DNA encoding Vernonia galamenensis fatty acid desaturase and fatty acid epoxidising enzyme - used to alter levels of expression of the enzymes in transformed host cells or to produce recombinant enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                      57 TFLLYTVANTYIPHLPPPLVYLAWPVYWFCQSCILTGLWVLGHECGHHAFSBYQWIDNAV 116
                                                                                                                                                                                                                                                                                                                                                                                                                  63 TPLLYTLANSYIPLLPPPLPYLAWPVYWFCQSSILTGLWVIGHECGHHAYSEYQWVDNTV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                             117 GFVLHSALLTPYFSWKYSHRKHHANTNSLENEEVYIPRTQSQLRTYSTYSFLDNTPGRIL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ILVIMLTLGFPLYLLTNVSGKKYDRFTNHFDPLSPIFTERERIQVALSDLGIVAVFYGLK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLVQTKGFGWVMCMYGVPVIGLNSFIIVITYLHHTHLSSPHYDSTEWNWIKGALTTIDRD 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FGLLNRVFHDVTHTHVLHHLFPY1PHYHAKEASEAIKPILGDYRMIDRTPFFKAMWREAK 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      enzyme. The present invention also describes: (i) Vernonia galamenensis fatty acid desaturase; (ii) chimeric genes comprising the fragments linked to regulatory sequences; and (iii) transformed host cells containing the chimeric genes. The DNA's from the present invention can be used to alter levels of expression of the enzymes in transformed host cells or to produce the recombinant enzymes by transformation of microbial host cells. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                 62
                                                                                                                                                                                                                                                                                                                                                                          3 MSDSCDDHDQLVKDDHNINERAPVDAAPFSLSDLKKAIPPHCFQRSAIRSSCYVVQDLII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FLVAKKGFGWVMRMYGAPVVGLNAFIIMITYLHHTHLSSPHYDSTEWNWIKGALTTIDRD
                                                                                                                                                                                                                                                                                                                                                             MSDSYDDR----MKDHDMDERAPIDPAPFSLSDLKKAIPAHCFRRSAVWSSCYVVQDLII
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                                                                                                                                                                                                  present sequence is Vernonia galamenensis fatty acid epoxidising
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                                                                                                                                                                                                                                                                                                                  Length 384;
                                                                                                                                                                                                                                                                                                                                        27; Indels
                                                                                                                                                                                                                                                                                                                  87.3%; Score 1821; DB 2;
84.3%; Pred. No. 5.3e-187;
                                                                                                                                                                                                                                                                                                                                       29; Mismatches
                                                            (DUPO ) DU PONT DE NEMOURS & CO E I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ECIYIEPDEDKKHKGVYWYHKM 384
                                                                                                                                                                             5; Col 29-32; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydroxylase/ epoxygenase, SEQ ID
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                    97US-00872302
                                         97US-00872302
                                                                                                                                                                                                                                                                                                                                        Matches 322; Conservative
                                                                                                    WPI; 1999-059065/05.
N-PSDB; AAV72550.
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                               Sequence 384 AA;
                    11-JUN-1997;
                                         11-JUN-11997;
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The present invention relates to transgenic plants (I) containing one or more DNA constructs have a nucleic acid encoding a protein effective for catalyzing the conversion of a substrate to a 16C, 18C or 20C monounsaturated fatty acid product, e.g. a fatty acid concounsaturated fatty acid product, e.g. a fatty acid encoding the protein, where the regulatory element operably linked to the nucleic acid encoding the protein, where the regulatory clement confers expression in vegetative tissue of the plant. The fatty clement confers expression in vegetative tissue of the plant. The fatty cacid epoxygenase or a fatty hydroxylase can be phospholipid:diacylglycerol acyltransferase (PDAGAT). (I) has an increased amount of hydroxylatty acid, e.g., ricinoleic acid and epoxy-fatty acid, e.g., vernolic acid, in a vegetative tissue. The DNA construct of (I) is useful in the production of hydroxylases and epoxygenases that controls nematode damage in commercially important plant species and so (I) exhibits increased resistance to mematodes. (I) provides an effective, environmentally safe methods of inhibiting nematode metabolism, growth, viability, development, infectivity and/or the nematode life cycle. (I) provides season-long nematode control, thus providing labor savings, by reducing the need for and frequency of chemical control. The present sequence is one such fatty acid epoxygenase and fatty hydroxylase used to illustrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 YTVANTYIPHLPPPLVYLAWPVYWFCQSCILTGLWVLGHECGHHAFSEYQWIDNAVGFVL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 HSALLTPYFSWKYSHRNHHANTNSLDNDEVYIPKRKSKVKIYS--KILNNPPGRVFTLVF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 MLTLGFPLYLLTNVSGKKYDRFTNHFDPLSPIFTERERIQVALSDLGIVAVFYGLKFLVQ 240
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Nematocide; Plant; 16C monounsaturated fatty acid; 18C monounsaturated fatty acid; 18C monounsaturated fatty acid; 20C monounsaturated fatty acid; 21c monounsaturated fatty acid epoxygenase; fatty hydroxylase; phospholipid:diacylglycerol; acyltransferase; DAAT; diacylglycerol; acyltransferase; DAAT; diacylglycerol; hydroxy-fatty acid; ricinoleic acid; epoxy-fatty acid; vernolic acid; nematode.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel transgenic plant containing DNA construct having nucleic acid encoding polypeptide for catalyzing conversion of substrate to monounsaturated fatty acid product, useful for controlling nematodes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Davila-Aponte JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
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Zentella R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 21; SEQ ID NO 36; 180pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2004; 2004WO-US003254.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-FEB-2003; 2003US-0445293P.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                             Stokesia laevis.
                                                                                                                                                                                                                                                                                                                                                                                                  WO2004071168-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nematocide; Plant; 16C monounsaturated fatty acid;
18C monounsaturated fatty acid; 20C monounsaturated fatty acid;
fatty acid epoxygenase; fatty hydroxylase; phospholipididiacylglycerol;
acyltransferase; PDAT; diacylglycerol; acyltransferase; DAGAT;
hydroxy-fatty acid; ricinoleic acid; epoxy-fatty acid; vernolic acid;
                season-long nematode control, thus providing labor savings, by reducing the need for and frequency of chemical control. The present sequence is one such farty acid epoxygenase and farty hydroxylase, which has been codon optimised for improved plant expression.
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development, infectivity and/or the nematode life cycle.
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                                                                                                                                                                            / Match 74.3%; Score 1549.5; DB 8
Local Similarity 72.0%; Pred. No. 9.8e-158;
Nes 272; Conservative 47; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Baublite C, Williams DJ,
Mclaird MB, Zentella R;
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                                                                                                                                    Sequence 377 AA;
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Hresko MC,
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                                                                                                                                                            300 NRVFHDVTHTHVLHHLISYIPHYHAKEARDAIKPVLGDYYKIDRTPIFKAMMREAKECIY 359
                                            | TKGFGMVMCMYGVPVIGLNSFIIVITYLHHTHLSSPHYDSTEWNWIKGALTTIDRDFGLL 300
                                                                         NRVFHDVTHTHVLHHLFPYIPHYHAKEASEAIKPILGDYRMIDRTPFFKAMWREAKECIY 360
  RLTLGFPLYLLTNISGKKYQRFANHFDPLSPIFTERERIQVLVSDLGLLAVIYAIKLLVA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nematocide, Plant, 16C monounsaturated fatty acid,
18C monounsaturated fatty acid, 20C monounsaturated fatty acid;
fatty acid epoxygenaes, fatty hydroxylase; phospholipid.cdiacylglycerol,
acylransferaes, PDAT; diacylglycerol, acylransferaes, DAGAT,
hydroxy-fatty acid, ricinoleic acid, epoxy-fatty acid, vernolic acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encoding polypeptide for catalyzing conversion of substrate to monounsaturated fatty acid product, useful for controlling nematodes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Codon optimised hydroxylase/ epoxygenase, SEQ ID 38.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 21, SEQ ID NO 38, 180pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zentella R;
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                                                                                                                                                                                                                                361 IEQDADSKHKGTYWYHKM 378
                                                                                                                                                                                                                                                          360 IEPDEDTEHKGVYWYHKM 377
                                                                                                                                                                                                                                                                                                                                                                                            ADR87357 standard; protein; 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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Mclaird MB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DIVE-) DIVERGENCE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2004-634973/61.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
    180
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ADR87357

LID ADR8

AAC ADR8

XXX ADR8

DJ L18-h

XXX ADR8

XXX COCH

ENCORMENT THE CO

359

Davila-Aponte JA;

Kloek AP,

06-OCT-2005 (first entry)

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The present invention relates to transgenic plants (1) containing one or more DNA constructs. The DNA constructs have a nucleic acid encoding a protein effective for catalyzing the conversion of a substrate to a 16C, 18C or 20C monounsaturated fatty acid product, e.g. a fatty acid concounsaturated fatty acid product, e.g. a fatty acid concounsaturated fatty acid product, e.g. a fatty acid concounsaturated encoding the protein, where the regulatory linked to the nucleic acid encoding the protein, where the regulatory clement confers expression in vegetative tissue of the plant. The fatty concounsation of a fatty hydroxylase can be prospholipidiacylglycerol acyltransferase (PDAT) or diacylglycerol acyltransferase (PDAT) or diacylglycerol acyltransferase (DAGAT). (1) has an increased amount of hydroxylasty acid, e.g., ricinoleic acid and epoxy-fatty acid, e.g., vernolic acid, in a vegetative tissue. The DNA construct of (1) is useful in the production of hydroxylases and epoxygenases that controls nematode damage in commercially important plant species and so (1) exhibits increased commercially important plant species and so (1) exhibits increased control, thus providing labor savings, by reducing development, infectivity and/or the nematode life cycle. (1) provides methods of inhibiting nematode metabolism, growth, viability, development, infectivity and/or the nematode life cycle. (1) provides canson. Inom mematode control, thus providing labor savings, by reducing the need for and frequency of chemical control. The present sequence is one such fatty acid epoxygenase and fatty hydroxylase, which has been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 MLTLGFPLYLLTNVSGKKYDRFTNHFDPLSPIFTERERIQVALSDLGIVAVFYGLKFLVQ 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 MSDLSDGK----NLLKRVPVDP-PFTLSDIKKAIPPHCFKRSVIRSSYYVVHDLIVSYVF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 AKGAVWVTCIYGVPVLGVSVFFVLITYLHHTHLSLPHYDSTEWNWIRGALSTIDRDFGFL
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                                                                                       Novel transgenic plant containing DNA construct having nucleic acid encoding polypeptide for catalyzing conversion of substrate to monounsaturated fatty acid product, useful for controlling nematodes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.3%; Score 1549.5; DB 8 72.0%; Pred. No. 9.8e-158; ive 47; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon optimised for improved plant expression.
                                                                                                                                                                               21; SEQ ID NO 42; 180pp; English
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Best Local Similarity 72.09
Matches 272; Conservative
                     2004-634973/61
                                           N-PSDB; ADR87352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 377 AA;
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AC AEC0
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The invention relates to a transgenic plant containing at least one DNA construct comprising: (a) a nucleic acid encoding a polypeptide effective for atalyzing the conversion of a substrate to a C16, C18, or C20 monounsaturated fatty acid product; and (b) a regulatory element operably linked to the nucleic acid encoding the polypeptide and conferring expression in a vegetative tissue of the plant. Also described: (1) a method of making a transgenic plant; (2) an isolated nucleic acid comprising the nucleotide sequence; (3) a recombinant nucleic acid comprising at least one regulatory element that confers expression in a vegetative tissue of a plant; and (4) a method of screening a transgenic plant for anthelmintic activity. The transgenic plant is useful in preparing compounds having anthelmintic activity. The exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 MLTLGFPLYLLTNVSGKKYDRFTNHFDPLSPIFTERERIQVALSDLGIVAVFYGLKFLVQ 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New transgenic plant having a DNA construct comprising a nucleic acid encoding a protein for catalyzing the conversion of a substrate to a Cl6, C18 or C20 monounsaturated fatty acid product, useful in preparing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MSDSYDDRMKDHDMDERAPIDPAPFSLSDLKKAIPAHCFRRSAVWSSCYVVQDLIITFLL
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                                                           transgenic plant; anthelmintic; epoxygenase.
                            Stokesia laevis epoxygenase SEQ ID NO:38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 21; SEQ ID NO 38; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                  Kloek AP, Da
Williams DJ;
                                                                                                                                                                                04-AUG-2004; 2004US-00912534.
                                                                                                                                                                                                             04-FEB-2004; 2004US-00772227.
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DAVILA-APONTE J
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anthelmintic compounds
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MB, Zentella
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MCLAIRD M B.
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WILLIAMS D J
                                                                                                                                                                                                                                             VERBSKY M L.
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Best Local Similarity
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                                                                                        Stokesia laevis
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(ZENT/)
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9 61 121

AEC02271

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Gaps

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Length 377;

61

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180 RLTLGFPLYLLTNISGKKYQRFANHFDPLSPIFTERERIQVLVSDLGLLAVIYAIKLLVA 239
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                                                                                                                                                                                                                                                                                                                                                                                               301 NRVFHDVTHTHVLHHLFPYIPHYHAKEASEAIKPILGDYRMIDRTPFFKAMWREAKECIY 360
                                                                                                                    7 MSDLSDGK----NLLKRVPVDP-PFTLSDIKKAIPPHCFKRSVIRSSYYVHDLIVSYVF
                                                                                                                                                                                                                                                                                                                                                                                                               240 AKGAVWVTCIYGVPVLGVSVPFVLITYLHHTHLSLPHYDSTEWNWIRGALSTIDRDFGFL
                                                                                                  1 MSDSYDDRMKDHDMDERAPIDPAPFSLSDLKKAIPAHCFRRSAVWSSCYVVQDLITFLL
                                       74.3%; Score 1549.5; DB 9; 72.0%; Pred. No. 9.8e-158; ive 47; Mismatches 52;
                                                                      Matches 272; Conservative
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WILLIAMS D J
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N-PSDB; AEC02260.
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KLOEK A P.
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                                                        Similarity
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             Sequence 377 AA;
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                                          Query Match
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(BAUB/)
(KLOE/)
(DAVI/)
(HRES/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a transgenic plant containing at least one DNA construct comprising: (a) a nucleic acid encoding a polypeptide effective for catalyzing the conversion of a substrate to a C16, C16, Or C20 monounsaturated fatty acid product; and (b) a regulatory element operably linked to the nucleic acid encoding the polypeptide and conferring expression in a vegetative tissue of the plant. Also described: (1) a method of maxing a transgenic plant; (2) an isolated nucleic acid comprising at least one regulatory element that confers expression in a vegetative tissue of a plant; and (4) a method of screening a transgenic plant for anthelmintic activity. The transgenic plant for anthelmintic activity. The transgenic plant is useful in preparing compounds having anthelmintic activity. The exemplification of the present invention.
                                            240 AKGAVWVTCIYGVPVLGVSVPFVLITYLHHTHLSLPHYDSTEWNWIRGALSTIDRDFGFL 299
                                                                                     NRVFHDVTHTHVLHHLFPYIPHYHAKEASEAIKPILGDYRMIDRTPFFKAMWREAKECIY 360
                                                                                                   New transgenic plant having a DNA construct comprising a nucleic acid encoding a protein for catalyzing the conversion of a substrate to a Cl6, Cl8 or C20 monounsaturated fatty acid product, useful in preparing
                             TKGFGWVMCMYGVPVIGLNSFIIVITYLHHTHLSSPHYDSTEWNWIKGALTTIDRDFGLL 300
180 RLTLGFPLYLLTNISGKKYQRFANHFDPLSPIFTERERIQVLVSDLGLLAVIYAIKLLVA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Davila-Aponte JA, Hresko MC;
                                                                                                                                                                                                                                                                                                                                                                        transgenic plant; anthelmintic; epoxygenase
                                                                                                                                                                                                                                                                                                                                          Stokesia laevis epoxygenase SEQ ID NO:42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 21; SEQ ID NO 42; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kloek AP, D. Williams DJ;
                                                                                                                                                                                                                                                   AEC02275 standard; protein; 377
                                                                                                                                                361 IEQDADSKHKGTYWYHKM 378
                                                                                                                                                                360 IEPDEDTEHKGVYWYHKM 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-AUG-2004; 2004US-00912534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-FEB-2004; 2004US-00772227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERBSKY M L.
BAUBLITE C.
KLOSK A P.
DAVILA-APONTE J A.
HRESKO M C.
                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Verbsky ML, Baublite C,
Molaird MB, Zentella R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anthelmintic compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WILLIAMS D J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2005-603337/62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZENTELLA R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AEC02266.
                                                                                                                                                                                                                                                                                                                                                                                                                                US2005172358-A1.
                                                                                                                                                                                                                                                                                                                                                                                                   Stokesia laevis.
                                                                                                                                                                                                                                                                                                             06-OCT-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-AUG-2005
                                                                                     301
                                                                                                                                                                                                                                                                                AEC02275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (VERB/)
(BAUB/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KLOE/)
(DAVI/)
(HRES/)
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                                                                                                                                                                                                                                     RESULT 8
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Hresko MC;
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Williams DJ;
                                                                                              transgenic plant; anthelmintic; epoxygenase.
                                                                                  Stokesia laevis epoxygenase SEQ ID NO:36.
                                            AEC02269 standard; protein; 377 AA
361 IEQDADSKHKGTYWYHKM 378
      360 IEPDEDTEHKGVYWYHKM 377
                                                                                                                                                  04-AUG-2004; 2004US-00912534.
                                                                                                                                                               04-FEB-2004; 2004US-00772227.
                                                                                                                                                                                               ä
                                                                      (first entry)
                                                                                                                                                                                                                                   ပ်ဆွဲ
                                                                                                                                                                                            DAVILA-APONTE J
                                                                                                                                                                                                                                   Baublite
Zentella
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The invention relates to a transgenic plant containing at least one DNA construct comprising: (a) a nucleic acid encoding a polypeptide effective for catalyzing the conversion of a substrate to a C16, C18, or C20 monounsaturated fatty acid product; and (b) a regulatory element operably linked to the nucleic acid encoding the polypeptide and conferring expression in a vegetative tissue of the plant. Also described: (1) a method of making a transgenic plant; (2) an isolated nucleic acid comprising the nucleotide sequence; (3) a recombinant nucleic acid construct comprising at least one regulatory element that confers expression in a vegetative tissue of a plant; and (4) a method of screening a transgenic plant for anthelmintic activity. The transgenic plant is useful in preparing compounds having anthelmintic activity. The present exemplification of the present invention.
                        ig a protein for catalyzing the conversion of a substrate to a C16, C20 monounsaturated fatty acid product, useful in preparing
  nucleic acid
     comprising a
  transgenic plant having a DNA construct
                                                                                                                           Claim 21; SEQ ID NO 36; 130pp; English.
                                                                        anthelmintic compounds.
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Sequence 377 AA;

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121 HSALLTPYFSWKYSHRKHHANTNSLENEEVYIPRTQSQLRTYSTYEFLDNTPGRILILVI 180
                                                                                                                                                                                                                                                                                                     MLTLGFPLYLLTNVSGKKYDRFTNHFDPLSPIFTERERIQVALSDLGIVAVFYGLKFLVQ 240
                                                                                                                                                                                                                                                                                                                          180 RLTLGFPLYLLTNISGKKYQRFANHFDPLSPIFTERERIQVLVSDLGLLAVIYAIKLLVA 239
                                                                                                                                                                                                                                                                                                                                                                              241 TKGFGWVMCMYGVPVIGLNSFIIVITYLHHTHLSSPHYDSTEWNWIKGALTTIDRDFGLL 300
                                                                                                                                                                                                                                                                                                                                                                                                                 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NRVFHDVTHTHVLHHLFPYIPHYHAKEASEAIKPILGDYRMIDRTPFFKAMWREAKECIY 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300 NRVFHDVTHTHVLHHLISYIPHYHAKEARDAIKPVLGDYYKIDRTPIFKAMMREAKECIY 359
                                                                                                                                                   61 YTVANTYIPHLPPPLVYLAWPVYWFCQSCILTGLWVLGHECGHHAFSEYQWIDNAVGFVL 120
                                                                                                                                                                        61
                                                                           1 MSDSYDDRMKDHDMDERAPIDPAPFSLSDLKKAIPAHCFRRSAVWSSCYVVQDLIITFLL 60
                                                                                                 7 MSDLSDGK----NLLKRVPVDP-PPTLSDIKKAIPPHCFKRSVIRSSYYVVHDLIVSYVF
                                                                                                                                                                                                                                                                                                                                                                                                               240 AKGAVWVTCIYGVPVLGVSVFFVLITYLHHTHLSLPHYDSTEWNWIRGALSTIDRDFGFL
                                      Gaps
                                    7;
74.3%; Score 1549.5; DB 9; Length 377; 72.0%; Pred. No. 9.8e-158; ive 47; Mismatches 52; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 IEQDADSKHKGTYWYHKM 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     360 IEPDEDTEHKGVYWYHKM 377
                                    Matches 272; Conservative
                   Best Local Similarity
                                                                                                                                                                                        62
                                                                                                                                                                                                                                                                                                     181
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 Query Match
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calendulic acid desaturase; unsaturated fatty acid; oil;

    C. officinalis calendulic acid desaturase.

                       AAB70946 standard; protein; 377 AA
                                                                                                                        triglyceride; transgenic plant
                                                                  (first entry)
                                                                                                                                              Calendula officinalis
                                                                                                                                                                   DE19941609-A1
                                                                  22-AUG-2001
                                                                                                              Calendula;
                                             AAB70946;
RESULT 10
                       PXSXXXXXXXXXXXXXX
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64 ANTYIPHLPPPLVYLAWPVYWFCQSCILTGLWVLGHECGHHAFSEYQWIDNAVGFVLHSA 123

124 LLIPYFSWKYSHRKHHANTNSLENEEVYIPRIQSQLRIYSTYEFLDNTPGRILILVIMLT

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6 RMSDPSEGKNILERVPVDP-PFTLSDLKKAIPTHCFERSVIRSSYYVVHDLIVAYVFYVL 8 RMKD----HDMDERAPIDPAPFSLSDLKKAIPAHCFRRSAVWSSCYVVQDLIITFLLYTV

124

64

7;

DB 4; Length 377;

Query Match 73.0%; Score 1523.5; DB 4; Best Local Similarity 71.7%; Pred. No. 6.3e-155; Matches 269; Conservative 45; Mismatches 54;

Sequence 377 AA;

243

184 LGFPLYLLTNVSGKKYDRFTNHFDPLSPIFTERERIQVALSDLGIVAVFYGLKFLVQTKG 183 LGFPLYLLTNISGKKYGRFANHFDPMSPIFNDRERVQVLLSDFGLLAVFYAIKLLVAAAKG

244 FGWVMCMYGVPVIGLNSFIIVITYLHHTHLSSPHYDSTEWNWIKGALTTIDRDFGLLNRV 303

243 AAWVINMYAIPVLGVSVFFVLITYLHTHISLPHYDSTEWNWIKGALSTIDRDFGFLNRV

304 FHDVTHTHVLHHLFPYIPHYHAKEASEAIKPILGDYRMIDRTPFFKAMWREAKECIYIEQ 363

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This invention describes a novel isolated nucleic acid sequence (I)
encoding a Calendula officinalis calendulic acid desaturase polypeptide.
CT the invention also describes (I) a process for producing unsaturated
fatty acids, comprising introducing at least one copy of (I) or (II) into
an oil-producing organism, growing the organism, isolating oil from the
corganism and releasing fatty acids from the oil; (2) a process for
producing triglycerides with an increased unsaturated fatty acid content,
comprising introducing at least one copy of (I) or (II) into an oil-
producing organism, growing the organism and isolating oil from the
corganism; (3) a process for producing saturated fatty acids, comprising
introducing at least one nonfunctional copy of (I) or (II) into an oil-
producing organism, growing the organism, isolating oil from the organism
crassing fatty acids from the oil; (4) a process for producing
crassing fatty acids from the oil; (4) a process for producing
crassing at least one nonfunctional copy of (I) or (II) into an oil-
croducing organism, growing the organism and isolating oil from the
crogranism; (5) an enzyme capable of converting a diunsaturated fatty acid
crassing the organism and isolating oil from the
crogranism; (5) an enzyme capable of converting a diunsaturated fatty acid
cof to a triunsaturated fatty acid. Transgenic organism
cof to a triunsaturated fatty acid. Transgenic organism;
colls with an increased unsaturated fatty acid content. Transgenic
                                                                                                                                                                                                                                                                                                                                               v nucleic acid sequence encoding Calendula officinalis calendulic acid
saturase, useful for e.g. producing transgenic plants having oil with
increased unsaturated fatty acid content,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organisms (especially plants) containing one or more nonfunctional copi of (I) are useful for producing oils with an increased saturated fatty acid content. (I) and fragments of (I) are also useful for isolating genomic sequences by homology screening. This sequence represents the calendulic acid desaturase described in the method of the invention
                                                                                                                                                                                                                       Ä
                                                                                                                                                                                                                       Peitzsch N,
                                                                                                                                                                                                                       Fritsche K,
                                                                                                                                                                       (IPBP-) IPB INST PFLANZENBIOCHEMIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1c; Page 15-16; 22pp; German.
                                                                       99DE-01041609
                                                                                                                       99DE-01041609
                                                                                                                                                                                                                       Hornung E,
                                                                                                                                                                                                                                                                       WPI; 2001-283028/30.
N-PSDB; AAF88311.
                                                                                                                                                                                                                                                                                                                                                     New nucleic acid
                                                                       01-SEP-1999;
                       08-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                               desaturase
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epoxygenated fatty acids. The invention includes genetically modified oil -accumulating organisms and to the oils derived from them. These oils can be used in production of coatings, resins, glues, plastics, surfactants or lubricants
                                                                                                                                                                                                                                     YFSWKYSHRKHHANTNSLENEEVYIPRTQSQLRTYSTYEFLDNTPGRILILVIMLTLGFP 187
                                                                                                                                                                                                                                                                                                                                    LYLLTNVSGKKYDRFTNHFDPLSPIFTERERIQVALSDLGIVAVFYGLKFLVQTKGFGWV 247
                                                                                                                                                                                                                                                                                                                                                                                         248 MCMYGVPVIGLNSFIIVITYLHHTHLSSPHYDSTEWNWIKGALTTIDRDFGLLNRVFHDV 307
                                                                                                                                                                                                                                                                                                                                                                                                        THTHVLHHLPPYIPHYHAKEASEAIKPILGDYRMIDRTPPFKAMWREAKECIYIEQDADS 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nematocide; Plant; 16C monounsaturated fatty acid;
18C monounsaturated fatty acid; 20C monounsaturated fatty acid;
fatty acid epoxygenae; fatty hydroxylase; phospholipid:diacylglycerol;
acyltransferase; PDAT; diacylglycerol; acyltransferase; DAGAT;
hydroxy-fatty acid; ricinoleic acid; epoxy-fatty acid; vernolic acid;
                                                                                                                                                                               IPHLPPPLVYLAWPVYWFCQSCILTGLWVLGHECGHHAFSEYQWIDNAVGFVLHSALLTP
                                                                                                                                                                                                                                                                                                                                                  8 RMKDHDMDERAPIDPAPFSLSDLKKAIPAHCFRRSAVWSSCYVVQDLIITFLLYTVANTY
                                                                                                                                       4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Davila-Aponte JA;
                                                                                                          Length 374;
                                                                                                        Query Match 72.4%; Score 1510; DB 2; Length 3. Best Local Similarity 70.4%; Pred. No. 1.8e-153; Matches 261; Conservative 50; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Williams DJ, Kloek AP,
Zentella R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Codon optimised hydroxylase/ epoxygenase, SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADR87360 standard; protein; 374 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-FEB-2004; 2004WO-US003254.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-FEB-2003; 2003US-0445293P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KHKGTYWYHKM 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Baublite C,
Mclaird MB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DIVE-) DIVERGENCE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2004071168-A2.
                                                                                  Sequence 374 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Crepis biennis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-AUG-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Verbsky ML,
Hresko MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                               128
                                                                                                                                                                                                                                                                                                                                                                                                                                                 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        368
                                                                                                                                                                                                                                                                                                                                    188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADR87360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nematode
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ADR87360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the amino acid sequence of a novel epoxygenase of a vernolic acid containing Crepis sp. (not crepis palaestina). It was deduced from lesolated CDNA clone Crepis (see AAV63102). The deduced sequence contains His-rich motifs (see AAM7972-54) that are characteristic of mixed function monooxygenases, and shows a high degree of homology to a novel delta-12-spoxygenase (see AAM79742) of C. palaestina. The invention relates generally to novel genetic sequences (see AAV63101-03) encoding fatty acid epoxygenases (see AAW79742-44), especially delta-12-epoxygenases or mixed function monooxygenases. These provide the means by which fatty acid metabolism can be manipulated in e.g. yeast, mould, bacteria, insects, birds, mammals and plants (especially oilseed plants such as flax), in particular to convert unsaturated fatty acids to
             Fatty acid epoxygenase, CrepX gene; delta-12-epoxygenase;
mixed function monooxygenase; epoxygenated fatty acid; transgenic plant;
vegetable oil; oilseed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated fatty acid epoxygenase gene - used particularly for transforming plants for producing modified oils for use in, e.g. coatings, resins, glues, plastics, surfactants or lubricants.
                                                                                                                                                                                                                                                                                                                                                                              /note= "His-rich region"
135. .139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              309. .313
/note= "His-rich region"
                                                                                                                                                                                                                                                                                                                                                                                                           /note= "His-rich region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lenman M;
                                                                                                                                                                                                                                                                                                                                                                                                                                    'notes "encoded by AGN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "encoded by GIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CSIR ) COMMONWEALTH SCI & IND RES ORG. (STYM/) STYMNE S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 29; Page 84-86; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                       AAW79743 standard; protein; 374 AA.
                                                                                                                                                                                                                                       Crepis sp. delta-12-epoxygenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97AU-00006226.
97US-0043706P.
97US-0050403P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Singh S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-AU000246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97AU-00006223
                                                                       DEDSEHKGVFWYHKM 377
                                                       DADSKHKGTYWYHKM 378
                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                    99. .104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stymne S, Green A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-568734/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAV63102
                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-APR-1997;
16-APR-1997;
20-JUN-1997;
                                                                                                                                                                                                            02-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9846762-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-OCT-1998
                                                                                                                                                                                                                                                                                                                           Crepis sp
                                                                                                                                                                                 AAW79743;
                                                        364
                                                                                  363
                             303
                                                                                                                                                                                                                                                                                                                                                     Key
Region
                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
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transgenic plant; anthelmintic; epoxygenase. Crepis biennis epoxygenase SEQ ID NO:41

04-AUG-2004; 2004US-00912534. 04-FEB-2004; 2004US-00772227.

US2005172358-A1. Crepis biennis Synthetic.

04-AUG-2005.

VERBSKY M L.

(VERB/)

BAUBLITE C. KLOEK A P.

> (KLOE/) (DAVI/) (HRES/)

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The present invention relates to transgenic plants (1) containing one or more DNA constructs. The DNA constructs have a nucleic acid encoding a protein effective for catalyzing the conversion of a substrate to a 16C, 18C or 20C monounsaturated fatty acid product, e.g. a fatty acid epoxygenase or a fatty hydroxylase, and a regulatory element operably confers expression in vegetative tissue of the plant. The fatty element confers expression in vegetative tissue of the plant. The fatty caid epoxygenase or a fatty hydroxylase can be controlly diacylglycerol acyltransferase (PDAT) or diacylglycerol acyltransferase (PDAT) is useful in the production of hydroxylases and epoxygenases that controls nematode damage in commercially important plant species and so (1) exhibits increased connection nematodes (1) provides and fevelopment, infectivity and/or the nematode life cycle. (1) provides control. The production connection mentalod control, thus providing labor savings, by reducing the need for and frequency of chemical control. The present sequence is codon optimised for improved plant expression.
                                                                                                               encoding polypeptide for catalyzing conversion of substrate to monounsaturated fatty acid product, useful for controlling nematodes
                                                                                  transgenic plant containing DNA construct having nucleic acid
                                                                                                                                                                                            Claim 21; SEQ ID NO 41; 180pp; English.
WPI; 2004-634973/61
                          N-PSDB; ADR87351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 374 AA;
                                                                                  Novel
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121 HSFLLTPYFSWKYSHRNHHANTSSIDNDEVYIPKSKSKLAL--TYKLLNNPPGRLLVWVI 178
                                                                                                                                                          YTVANTYIPHLPPPLVYLAWPVYWFCQSCILTGLWVLGHECGHHAFSEYQWIDNAVGFVL 120
                                                                                                                                                                                                                                   HSALLTPYFSWKYSHRKHHANTNSLENEEVYIPRTQSQLRTYSTYEFLDNTPGRILILVI 180
                                                                                                                                                                                                                                                                                                          MLTLGFPLYLLTNVSGKKYDRFTNHFDPLSPIFTERERIQVALSDLGIVAVFYGLKFLVQ 240
                                                                                                                                                                                                                                                                                                                                179 MFTLGFPLYLLTNISGKKYDRFANHFDPMSPIFKERERFQVLLSDLGLLAVFYGIKVAVA 238
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                                                                                                                                                                                                                                                                                                                                                                                                           239 KKGAAWVACMYGVPMLGVFTLFDIITYLHHTHQSSPHYDSTEWNWIRGALSAIDRDFGFM 298
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                                                                               9
                                                                                                    1 MSDSYDDRAMKDHDMDERAPIDPAPFSLSDLKKAIPAHCFRRSAVWSSCYVVQDLIITFLL
                                         Gaps
                                         4;
72.1%; Score 1504; DB 8; Length 374; 69.0%; Pred. No. 7.9e-153; ive 50; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 IEQDADSKHKGTYWYHKM 378
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                     Best Local Similarity 69.0%
Matches 261; Conservative
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New transgenic plant having a DNA construct comprising a nucleic acid encoding a protein for catalyzing the conversion of a substrate to a C16, C18 on C20 monounsaturated fatty acid product, useful in preparing anthelmintic compounds.

Claim 21; SEQ ID NO 41; 130pp; English

Hresko MC;

Davila-Aponte JA,

Kloek AP, Da Williams DJ;

υ'n

Baublite ( Zentella F

ME,

Verbsky N Mclaird N

2005-603337/62.

N-PSDB; AEC02265

DAVILA-APONTE J P HRESKO M C. MCLAIRD M B.

ZENTELLA R. WILLIAMS D J.

(ZENT/) (WILL/)

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The invention relates to a transgenic plant containing at least one DNA construct comprising: (a) a nucleic acid encoding a polypeptide effective for catalyzing the conversion of a substrate to a C16, C18, or C20 monoumsaturated fatty acid product; and (b) a regulatory element operably linked to the nucleic acid encoding the polypeptide and conferring expression in a vegetative tissue of the plant. Also described: (1) a method of making a transgenic plant; (2) an isolated nucleic acid comprising the nucleotide sequence; (3) a recombinant nucleic acid construct comprising at least one regulatory element that confers expression in a vegetative tissue of a plant; and (4) a method of screening a transgenic plant for anthelmintic activity. The transgenic plant is useful in preparing compounds having anthelmintic activity. The exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 YTVANTYIPHLPPPLVYLAWPVYWFCQSCILTGLWVLGHECGHHAFSEYQWIDNAVGFVL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MSDSYDDRMKDHDMDERAPIDPAPFSLSDLKKAIPAHCFRRSAVWSSCYVVQDLIITFLL
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69.0%; Pred. No. 7.9e-153;
iive 50; Mismatches 63;
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Matches 261; Conservative
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AEC02274 standard; protein; 374 AA.

06-OCT-2005 (first entry)

AEC02274;

RESULT 13
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Hresko MC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New tranagenic plant having a DNA construct comprising a nucleic acid encoding a protein for catalyzing the conversion of a substrate to a C16, C18 or C20 monounsaturated fatty acid product, useful in preparing
                                            239 KKGAAWVACMYGVPMLGVFTLFDIITYLHHTHQSSPHYDSTEWNWIRGALSAIDRDFGFM 298
                                                                                   NRVFHDVTHTHVLHHLFPYIPHYHAKEASEAIKPILGDYRMIDRTPFRAMWREAKECIY 360
                                                                                                  TKGFGWVMCMYGVPVIGLNSFIIVITYLHHTHLSSPHYDSTEWNWIKGALTTIDRDFGLL 300
179 MFTLGFPLYLLTNISGKKYDRFANHFDPMSPIFKERERFQVLLSDLGLLAVFYGIKVAVA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Davila-Aponte JA, Hresko MC;
                                                                                                                                                                                                                                                                                                                                                             transgenic plant; anthelmintic; epoxygenase
                                                                                                                                                                                                                                                                                                                                  Crepis biennis epoxygenase SEQ ID NO:137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 21; SEQ ID NO 137; 130pp; English.
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                                                                                                                                                                                                                                            AEC02370 standard; protein; 374
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Mclaird MB, Zentella R,
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HRESKO M C.
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WILLIAMS D J.
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KLOEK A P.
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                                                                                                                                                                                                                                                                                                                                                                                                                 301 NRVFHDVTHTHVLHHLFPYIPHYHAKEASEAIKPILGDYRMIDRTPFFKAMWREAKECIY 360
                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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18C monounsaturated fatty acid; 20C monounsaturated fatty acid;
fatty acid epoxygenae; fatty hydroxylase; phospholipid.diacylglycerol;
acyltransferase; PDAT; diacylglycerol; acyltransferase; DAGAT;
hydroxy-fatty acid; ricinoleic acid; epoxy-fatty acid; vernolic acid;
                                                                                                                 1 MASSCHSKTSKKSVMERVSVDPVPFSLSDLKQAIPPHCFQRSVIRSSYYVVHDLIIAYIF
                                                                                                                                                       61 YTVANTYIPHLPPPLVYLAWPVYWFCQSCILTGLWVLGHEGGHHAFSEYQWIDNAVGFVL
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                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel transgenic plant containing DNA construct having nucleic acid encoding polypeptide for catalyzing conversion of substrate to
                                                             4
                            Length 374;
                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Williams DJ, Kloek AP,
Zentella R;
                          71.9%; Score 1499; DB 9; 68.8%; Pred. No. 2.7e-152; ive 51; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hydroxylase/ epoxygenase, SEQ ID 18
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                                            Best Local Similarity 68.89
Matches 260; Conservative
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Mclaird MB,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-634973/61.
                                         Similarity
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Sequence 374 AA;
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The present invention relates to transgenic plants (I) containing one or more DNA constructs. The DNA constructs have a nucleic acid encoding a protein effective for catalyzing the conversion of a substrate to a 16C, 18C or 20C monounsaturated fatty acid product, e.g. a fatty acid epoxygenase or a fatty hydroxylase, and a regulatory element operably linked to the nucleic acid encoding the protein, where the regulatory element confers expression in vegetative tissue of the plant. The fatty acid epoxygenase or a fatty hydroxylase can be phospholipid:diacylglycerol acyltransferase (PDAT) or diacylglycerol acyltransferase (PDAT) or diacylglycerol acyltransferase (DAAT). (I) has an increased amount of hydroxy-fatty acid, e.g., vernolic acid, in a vegetative tissue. The DNA construct of (I) is useful in the production a vegetative tissue. The DNA construct of (I) is useful in the production of hydroxylases and epoxygenases that controls nematod elamage in commercially important plant species and so (I) exhibits increased resistance to nematodes. (I) provides an effective, environmentally safe methods of inhibiting nematode metabolism, growth, viability, casistance to nematode control, thus providing labor savings, by reducing the need for and frequency of chemical control. The present sequence is one such fatty acid epoxygenase and fatty hydroxylase used to illustrate
monounsaturated fatty acid product, useful for controlling nematodes.
                                                        Claim 21; SEQ ID NO 18; 180pp; English.
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Sequence 374 AA;

196 GKKYDRFTNHFDPLSPIFTERERIQVALSDLGIVAVFYGLKFLVQTKGFGWVMCMYGVPV 255 254 LGVFTLFDIITYLHHTHQSSPHYDSTEWNWIRGALSAIDRDFGFMNSVFHDVTHTHVMHH 313 314 MPSYIPHYHAKEARDAINTIIGDYYMIDRTPILKALWREAKECMYIE--PDSKRKGVYWY 371 76 VYLAWPVYWFCQSCILTGLWVLGHECGHHAFSEYQWIDNAVGFVLHSALLTPYFSWKYSH 135 RKHHANTNSLENEEVYIPRTQSQLRTYSTYBFLDNTPGRILLILVIMLTLGFPLYLLTNVS 195 IGLNSFIIVITYLHHTHLSSPHYDSTEWNWIKGALTTIDRDFGLLNRVFHDVTHTHVLHH 315 LFPYIPHYHAKBASEAIKPILGDYRMIDRTPFFKAMWREAKECIYIEQDADSKHKGTYWY 375 16 ERAPIDPAPFSLSDLKKAIPAHCFRRSAVWSSCYVVQDLIITFLLYTVANTYIPHLPPPL 4; Gaps. 71.8%; Score 1498; DB 8; Length 374; 71.1%; Pred. No. 3.5e-152; ive 48; Mismatches 53; Indels 4 Best Local Similarity 71.1 Matches 258; Conservative HKM 378 316 376 136 256 Query Match g ઠે 셤 ò g ઠે g ઠે 셤 ઠે a ò

Search completed: September 22, 2006, 19:38:16 Job time : 201 secs

HKL 374

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TYPE: prt
ORGANISM: Glycine max
FEATURE:
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Sequence 75575, A
Sequence 98547, A
Sequence 109786,
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39928, A
42536, A
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Sequence 43123, A
Sequence 28921, A
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                                                                                                                                           2 ; Search time 34 Seconds
(without alignments)
791.157 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/EMC Celerra SIDS3/ptodata/2/pubpaa/US09_NEW PUB.pep:*
/EMC Celerra SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/EMC Celerra SIDS3/ptodata/2/pubpaa/US07_NEW PUB.pep:*
/EMC Celerra SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/EMC Celerra SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/EMC Celerra SIDS3/ptodata/2/pubpaa/US10_NEW PUB.pep:*
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/EMC Celerra SIDS3/ptodata/2/pubpaa/US11_NEW PUB.pep:*
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Sequence 399
Sequence 429
                         GenCore version 5.1.9
(c) 1993 - 2006 Biocceleration Ltd.
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US-11-056-355B-3929

US-11-056-355B-75575

US-11-056-355B-98547

US-11-056-355B-98547

US-11-056-355B-3928

US-11-056-355B-3928

US-11-056-355B-3928

US-11-056-355B-39546

US-11-056-355B-28876

US-11-056-355B-28875

US-11-056-355B-2865

US-11-056-355B-28875

US-11-056-355B-2865

US-11-058-746-5

US-11-340-318-4
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US-10-449-902-43123
US-10-953-349-28921
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                                                                                                                                                                                                                                                                                                                                                                        260401 segs, 71162236 residues
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                                                                                                                                           September 22, 2006, 19:56:22
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Maximum Match 100%
Listing first 45 summaries
                                                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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2086
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Maximum DB
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Result No.

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Sequence 52712, Application US/11056355B

Sequence 52712, Application No. US20060150283A1

GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav

TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding

TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding

TITLE OF INVENTION: Polypeptides Encoded Thereby

FILE REFERENCE: 2750-1590F052

CURRENT APPLICATION NUMBER: US/11/056,355B

CURRENT FILING DATE: 2008-02-14

PRIOR FILING DATE: 2004-02-13

NUMBER OF SEQ ID NOS: 119966

SEQ ID NO 52712
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28920, A
38515, A
1518, A
15195, A
15295, A
15294, A
15274, A
15294, A
38513, A
38513, A
15293, A
36480, A
36360, A
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9, Appli
28922, A
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Local Similarity 58.1%; Pred. No. 7.5e-108;
hes 215; Conservative 66; Mismatches 87; Indels
                                                  US-11-056-355B-5958
US-11-056-355B-15295
US-10-953-35B-1517
US-11-056-355B-1517
US-11-056-355B-15294
US-10-056-355B-15294
US-10-953-349-38513
US-11-056-355B-15293
US-11-056-355B-15293
US-11-056-355B-15293
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US-11-056-355B-15293
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US-11-056-355B-3680
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US-10-953-349-28922
US-11-058-746-8
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| LOCATION: (1)...(383)
| OTHER INFORMATION: Ceres Seq. ID no. 15177299
| US-11-056-3558-52712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68 FSLLPQPLSYLAWPLYWACQGCVLTGIWVIAHECGHHAFSDYQWLDDTVGLIFHSFLLVP 127
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68 IPHLPPPLVYLAMPVYWFCQSCILTGLWVLGHECGHHAFSEYQWIDNAVGFVLHSALLTP 127
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APPLICANT: Brover, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590F082
CURRENY APPLICATION NUMBER: US/11/056,355B
CURRENY FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 39929
LENGTH: 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             | PEATURE:
| NAMEX/KEY: peptide
| LOCATION: (1)..(377)
| OTHER INFORMATION: Ceres Seq. ID no. 12370301
| US-11-056-3558-39929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 42537, Application US/11056355B Publication No. US20060150283A1 GENERAL INFORMATION:
                                                                                                                                                                Sequence 39929, Application US/11056355B Publication No. US20060150283A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: prt
ORGANISM: Arabidopsis thaliana
                                                                   371 TESKGVFWYN 380
                                                 SKHKGTYWYH 376
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US-11-056-355B-42537
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Sequence 75575, Application US/11056355B
; Publication No. US20060150283A1
; GENREAL INFORMATION:
; APPLICANT: Brover, Vacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REPRENCE: 2756-1590P052
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; RIOR APPLICATION NUMBER: 60/544,190
; RIOR APPLICATION NUMBER: 60/544,190
; RIOR APPLICATION NUMBER: 119966
; SEQ ID NO 75575
; LEMGTH: 377
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | SECTION | SECT
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OP INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OP INVENTION: Bolypeptides Encoded Thereby
FILE REPERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR PILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 42537
LENGTH: 377
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55.6%; Pred. No. 1.8e-103;
tive 70; Mismatches 92;
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; OTHER INFORMATION: Ceres Seq. ID no. 12337752
US-11-056-355B-42537
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ORGANISM: Arabidopsis thaliana
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Best Local Similarity 55.69
Matches 205; Conservative
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128 YFSWKYSHRKHHANTNSLENEEVYIPRTOSOLRTYSTYBFLDNTPGRILLILVIMLTLGFP 187
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FSLLPQPLSYLAWPLYWACQGCVLTGIWVIAHECGHHAFSDYQWLDDTVGLIFHSFLLVP 127
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APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 109786
LENGTH: 377
                                                                                                        188 LYLLTNVSGKKYDRFTNHFDPLSPIFTERERIQVALSDLGIVAVFYGLKFLVQTKGFGWV
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55.6%; Pred. No. 1.8e-103;
tive 70; Mismatches 92; Indels
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LOCATION: (1)..(377)

MATERIAN: INFORMATION: Ceres Seq. ID no. 13600978

US-11-056-3558-109786
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ORGANISM: Arabidopsis thaliana
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Best Local Similarity 55.64
Matches 205, Conservative
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                                                                                                                                                                          Length 377;
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Publication No. US20060150283A1
GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments;
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENT POLYPEPTION: POLYPEPTIONS
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 98547
                                                                                                                                                                      58.2%; Score 1215; DB 7;
55.6%; Pred. No. 1.8e-103;
iive 70; Mismatches 92;
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; LOCATION: (1)..(377)
; OTHER INDEMATION: Ceres Seq. ID no. 13600978
US-11-056-355B-98547
      ; LUCATION: (1)..(377)
; OTHER INFORMATION: Ceres Seq. ID no. 6444002
US-11-056-3558-75575
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ORGANISM: Arabidopsis thaliana
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Best Local Similarity 55.68
Matches 205; Conservative
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APPLICANT: Brover, Vickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REPERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR PILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 39928
LENGTH: 383
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APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
TITLE OF INVENTION: Polypeptides Encoded Thereby
CURRENT S-756-1250PUS2
CURRENT APPLICATION NUMBER: 18/11/056,355B
CURRENT FILING DATE: 2005-02-14
FRICA APPLICATION NUMBER: 60/544,190
FRICA PAPLICATION DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRATURE:
NAMEKKEY: peptide
LOCATION: (1)..(383)
OTHER INFORMATION: Ceres Seq. ID no. 12370300
US-11-056-355B-39928
                                         Sequence 39928, Application US/11056355B Publication No. US20060150283A1 GENERAL INFORMATION:
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; Publication No. US20060150283A1
; GENERAL INFORMATION:
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ORGANISM: Arabidopsis thaliana
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APPLICANT: Van de Loo, Frank
APPLICANT: Van de Loo, Frank
APPLICANT: Won de Loo, Frank
TILLE OF INVENTION: PLANTS
TITLE OF INVENTION: PLANTS
FRIOR FILING DATE: 1996-02-06
PRIOR PLICATION NUMBER: US 08/530,862
PRIOR PLICATION NUMBER: US 08/530,982
PRIOR FILING DATE: 1994-10-11
PRIOR PLILING DATE: 1994-10-11
PRIOR PLILING DATE: 1994-10-11
PRIOR PLILING DATE: 1994-10-11
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68 IPHLPPPLVYLAWPVYWFCQSCILTGLWVLGHECGHHAFSEYQWIDNAVGFVLHSALLTP 127
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55.6%; Pred. No. 1.9e-103;
tive 70; Mismatches 92;
                                                                                                                                                                                                                                                 Sequence 6, Application US/11058746, Publication No. US20060101543A1, GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.3
SEQ ID NO ELENGTH: 383
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Matches 205; Conservative
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Publication No. US20060150283A1
GRERAL INFORMATION:
GRERAL INFORMATION:
APPLICANT: Brower, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
FILE REFERENCE: 2750-1596Pgides Encoded Thereby
FILE REFERENCE: 2750-1596Pgides
CURRENT APPLICATION NUMBER: US/11/056,355B
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Best Local Similarity 55.6%; Pred. No. 1.9e-103;
Matches 205; Conservative 70; Mismatches 92;
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55.6%; Pred. No. 1.9e-103;
tive 70; Mismatches 92;
                                                                   NAME/KEY: peptide
LOCATION: (1). (1883)
1 DOCATION: (1). (1883)
2 THER INDEMALION: Ceres Seq. ID no. 12337751
US-11-056-355B-42536
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; OTHER INFORMATION: Ceres Seq. ID no. 6444001
US-11-056-3558-75574
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PRIOR PILING DATE: 2004-02-13
                           TYPE: prt
ORGANISM: Arabidopsis thaliana
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ORGANISM: Arabidopsis thaliana
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SEQ ID NO 75574
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Matches 205; Conservative
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NAME/KEY: peptide
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US-11-056-3558-75574
SEQ ID NO 42536
LENGTH: 383
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APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT FPLINGNION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2004-02-14
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 98546
LENGTH: 383
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55.6%; Pred. No. 1.9e-103;
:ive 70; Mismatches 92;
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| NAME/KEY: peptide
| LOCATION: (1)..(383)
| OTHER INFRANTION: Ceres Seq. ID no. 13600977
| US-11-056-355B-98546
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ORGANISM: Arabidopsis thaliana
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Best Local Similarity 55.6%
Matches 205; Conservative
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MCMYGVPVIGLNSFIIVITYLHHTHLSSPHYDSTEWNWIKGALTTIDRDFGLLNRVFHDV 307
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APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: BOUNDED BE Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR PILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 109785
LENGTH: 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEATURE:
NAME/KEY: peptide
LOCATION: (1)..(383)
LOCATION: (1)..(383)
VS-11-056-355B-109785
                                                                                                                                                                                                                  ; Sequence 109785, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Arabidopsis thaliana
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Best Local Similarity 55.6%
Matches 205; Conservative
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                                                                                                                  368 KHKGTYWYH 376
                                                                                                                                          372 DKKGVYWYN 380
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US-11-056-355B-109785
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RESULT 13 US-11-056-355B-28876

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Sequence 28876, Application US/11056355B
Publication No. US20060150283A1
GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590F082
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR PPLICATION NUMBER: 60/544,190
PRIOR PLICATION NUMBER: 60/544,190
PRIOR PLICATION NUMBER: 60/544,190
PRIOR PLING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 28876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 IPHLPPPLVYLAWPVYWFCQSCILTGLWVLGHECGHHAFSEYQWIDNAVGFVLHSALLTP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 YFSWKYSHRKHHANTNSLENEEVYIPRTQSQLRTYSTYBFLDNTPGRILLILVIMLTLGFP 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188 LYLLTNVSGKKYDRFTNHFDPLSPIFTERERIQVALSDLGIVAVFYGLKFLVQTKGFGWV 247
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APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REPERBNCE: 276-1590F082
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT APPLICATION NUMBER: 60/544,190
PRIOR PLING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 32466
LENGTH: 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 58.2%; Score 1214; DB 7; Best Local Similarity 55.6%; Pred. No. 2.36-103; Matches 205; Conservative 69; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1)...(377)
; OTHER INFORMATION: Ceres Seq. ID no. 12321217
US-11-056-3558-28876
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; Sequence 32466, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: prt
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           368 KHKGTYWYH 376
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68 IPHLPPPLVYLAWPVYWFCQSCILTGLWVLGHECGHHAFSEYQWIDNAVGFVLHSALLTP

187

247

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128 YFSWKYSHRRHHSNTGSLERDEVFVPKQKSAIKWYGKY--LNNPLGRIMMLTVQFVLGWP 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Brover, Vyacheslav
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION WUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR APPLICATION NUMBER: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 28875
                                                                                                                                                                                                                                      68 IPHLPPPLVYLAWPVYWFCQSCILTGLWVLGHECGHHAFSEYQWIDNAVGFVLHSALLTP
                                                                                                                                                                                                            8 RMKDHDMDERAPIDPAPFSLSDLKKAIPAHCFRRSAVWSSCYVVQDLIITFLLYTVANTY
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                                                                                                                                   Length 377;
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; Pred. No. 2.3e-103;
69; Mismatches 93;
                                                                                                                                     Score 1214; DB 7;
Pred. No. 2.3e-103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (1)..(383)
; OTHER INFORMATION: Ceres Seq. ID no. 12321216
US-11-056-3558-28875
                                                                              ID no. 12321217
                                                                                                                                                                       69; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 28875, Application US/11056355B Publication No. US20060150283A1 GENERAL INFORMATION:
ORGANIŠM: Arabidopsis thaliana FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: prt
ORGANISM: Arabidopsis thaliana
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                                                           ; LOCATION: (1)..(377)
; OTHER INFORMATION: Ceres Seq.
US-11-056-355B-32466
                                                                                                                                     58.2%;
                                                                                                                                 Query Match
Best Local Similarity 55.65
Matches 205; Conservative
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Best Local Similarity 55.6
Matches 205; Conservative
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                                           NAME/KEY: peptide
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US-11-056-355B-28875
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192 LYLAFNVSGRPYDGFACHFFPNAPIYNDRERLQIYLSDAGILAVCFGLYRYAAAQGMASM 251
                                                                                                                                                                       248 MCMYGVPVIGLNSFIIVITYLHHTHLSSPHYDSTEWNWIKGALTTIDRDFGLLNRVFHDV 307
                                                                                                                                                                                                                                    308 THTHVLHHLFPYIPHYHAKEASEAIKPILGDYRMIDRTPFFKAMWREAKECIYIEQDADS 367
                                                                                                                                                                                                                                                     312 TDTHVAHHLFSTMPHYNAMEATNAIKPILGDYYQPDGTPWYVAMYREAKECIYVEPDREG 371
                                            YFSWKYSHRKHHANTNSLENEEVYIPRTQSQLRTYSTYEFLDNTPGRILILVIMLTLGFP
                                                                                                        188 LYLLTNVSGKKYDRFTNHFDPLSPIFTERERIQVALSDLGIVAVFYGLKFLVQTKGFGWV
                                                                                                                                                                                         completed: September 22, 2006, 19:59:58
                                                                                                                                                                                                                                                                                                  368 KHKGTYWYH 376
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GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

September 22, 2006, 19:38:36; Search time 42 Seconds (without alignments) 865.951 Million cell updates/sec Run on:

1 MSDSYDDRMKDHDMDERAPI.....IYIEQDADSKHKGTYWYHKM 378 US-10-622-774-2 2086 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_80:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

omega-6 desaturase omega-6 desaturase Delta12 fatty acid oleate 12-hydroxyl fungal elicitor-in omega-6 fatty acid stearoyl-CoA 9-des omega-3 fatty acid stearoyl-CoA 9-des probable omega-3 f Delta12 fatty acid omega-6 fatty acid omega-6 desaturase Description SUMMARIES T109880 T14269 T109839 T15043 T107687 T07009 AG2005 AG2005 T15039 T110063 T01696 J02339 JC2555 J02335 T01697 J02336 J02337 T10898 T07688 T10789 Query Match Length DB 601 594.5 594.5 594 593.5 588.5 Result No. 

omega-3 fatty acid	omega-3 tatty acid	omega-3 fatty acid	hypothetical prote	omega 6 desaturase	phosphatidylcholin	phosphatidylcholin	phosphatidylcholin	phosphatidylcholin	phosphatidylcholin	hypothetical prote	n-6 fatty acid des	probable omega-6 d	omega-6 desaturase	Deltal2 fatty acid	fatty-acid desatur
T06238	S52650	T06235	T26075	JC5891	S11519	S43770	S43772	AH2005	S43771	D85362	853309	T08136	T07742	S54259	B69901
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383	359	380	376	424	351	349	350	350	347 2	448 2	447 2	443 2	424 2	351 2	352
27.7 383 2				-											
	27.5		20.7	16.5	14.8	14.7		14.3	14.3		13.6	13.5	13.3		10.5

## ALIGNMENTS

RESULT 1 T10480 Delta12 fatty acid de Delta12 fatty acid de C;Species: Solanum con C;Date: 16-Jul-1999 # C;Accession: T10480 R;Consiglio, F; Amat submitted to the EMBL A;Reference number: Z A;Accession: T10480 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-383 <co a;cross-references:="" a;experimental="" c;reywords:="" c;superfamily:="" fatty="" oxidoredu<="" source="" th="" u=""><th>desaturase (EC 1.14.99) [imported commersonis (Commerson's wild potat #sequence_revision 16-Jul-1999 #teatuda, M.R.; Leone, A.; Costa, A.; EL Data Library, November 1995 217044  ry; translated from GB/EMBL/DDBJ NA NA CONTROT:Q41305; UNIPARC:UPI0000033 ce: clone ScDes D111  y acid (acyl-COA) desaturase ductase; unsaturated fatty acid bio</th></co>	desaturase (EC 1.14.99) [imported commersonis (Commerson's wild potat #sequence_revision 16-Jul-1999 #teatuda, M.R.; Leone, A.; Costa, A.; EL Data Library, November 1995 217044  ry; translated from GB/EMBL/DDBJ NA NA CONTROT:Q41305; UNIPARC:UPI0000033 ce: clone ScDes D111  y acid (acyl-COA) desaturase ductase; unsaturated fatty acid bio
Query Match Best Local Matches 21	Query Match 60.9%; Score 1271; DB 2; Length 383; Best Local Similarity 58.3%; Pred. No. 2.7e-99; Matches 210; Conservative 67; Mismatches 81; Indels 2; Gaps 1;
Qy da	16 ERAPIDPAPFSLSDLKKAIPAHCFRRSAVWSSCYVVQDLIITFLLYTVANTYIPHLPPPL 75 ::
oy G	76 VYLAWPVYWFCQSCILTGLWVLGHECGHHAFSEYQWIDNAVGFVLHSALLTPYFSWKYSH 135
0y 1	136 RKHHANTNSLENEEVYIPRTOSOLRTYSTYEFLDNIPGRILILVIMLTLGFPLYLLINVS 195 
Oy . 1	196 GKKYDRFTNHFDPLSPIFTERERIOVALSDLGIVAVFYGLKFLVOTKGFGWVMCMYGVPV 255 
0y 2	256 IGLNSFIIVITYLHHTHLSSPHYDSTEWNWIKGALTTIDRDFGLLNRVFHDVTHTHVLHH 315 ::  ::
Oy 3	316 LEPYIPHYHAKEASEAIKPILGDYRWIDRTPFKAMWREAKECIYIEQDADSKHKGTYWY 375 

T15042 omega-6 fatty acid desaturase (EC 1.14.99.-) - parsley C.Species: Petroselinum crispum (parsley) C.Spate: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004 RESULT 2

omega-3 fatty acid omega-3 fatty acid omega-3 fatty acid

PQ0812 A44227

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C;Species: Gossturase, microsomal - upland cotton
C;Species: Gossypium hirsutum (upland cotton)
C;Species: Gossypium hirsutum (upland cotton)
C;Accession: T0789
R;Liu, Q.; Singh, S.P.; Green, A.; Sharp, P.J.; Marshall, D.R.
Submitted to the EMBL Data Library, March 1999
R;Diu, Q.; Singh, S.P.; Green, A.; Sharp, P.J.; Marshall, D.R.
A;Description: Isolation and characterisation of two different microsomal omega-6 desatum
A;Reference number: Z17145
A;Accession: T10789
A;Accession: T10789
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: preliminary;
A;Molecule type: mRNA
A;Residues: 1-383 <LIU>
A;Cross-references: UNIPPROT: O23956; UNIPARC: UPI00000A24F4; EMBL: Y10112
A;Experimental source: subspecies Deltapine-16
C;Function: innolled in production of an accession of a production of a produc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  311 ITDTHVAHHLFSTMPHYHAMEATKAIKPILGEYYRFDETPFVKAMWRBARECIYVEPDQS 370
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                                                                                                                                    VMCMYGVPVIGLNSFIIVITYLHHTHLSSPHYDSTEWNWIKGALTTIDRDFGLLNRVFHD 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         307 VTHTHVLHHLFPYIPHYHAKEASEAIKPILGDYRMIDRTPFFKAMWREAKECIYIEQDAD 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 IGLNSFIIVITYLHHTHLSSPHYDSTEWNWIKGALTTIDRDFGLLNRVFHDVTHTHVLHH
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DRMKDHDMDERAPIDPAPFSLSDLKKAIPAHCFRRSAVWSSCYVVQDLIITFLLYTVANT
                                                                                                             67 YIPHLPPPLVYLAMPVYWFCQSCILTGLWVLGHECGHHAFSEYQWIDNAVGFVLHSALLT
                                                                                                                                                                                                                    PYFSWKYSHRKHHANTNSLENEEVYIPRTQSQLRTYSTYEFLDNTPGRILILVIMLTLGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Description: involved in production of polyunsaturated lipids C; Superfamily: fatty acid (acyl-CoA) desaturase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 58.8%; Score 1226; DB 2; Length 3 Best Local Similarity 56.9%; Pred. No. 1.7e-95; Matches 205; Conservative 72; Mismatches 81; Indels
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C;Accession: T15042
R;Kirsch, C.; Hahlbrock, K.; Somssich, I.E.
Plant Plant Sand. 115, 283-289, 1997
A;Title: Rapid and transient induction of a parsley microsomal delta 12 fatty acid desath A;Title: Rapid and transient induction of a parsley microsomal delta 12 fatty acid desath A;Reference number: 218274; MUID:97451781; PMID:9306702
A;Accession: T15042
A;Accession: T15042
A;Residue: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-382 <KIRA
A;Residues: 1-382 <KIRA
A;Cross-references: UNIPROT:024471; UNIPARC:UPI00000A6333; EMBL:U86072; NID:g2501789; PIC;Superfamily: fatty acid (acyl-CoA) desaturase
C;Ksywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RKHHANTNSLENEEVYIPRIQSQLRTYSTYEFLDNTPGRILLILVIMLTLGFPLYLLTNVS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198
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CiSpecies Glycine may-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
CiAccession: T07688
R;Heppard, E.P.; Kinney, A.J.; Stecca, K.L.; Miao, G.H.
Plant Physiol. 110, 311-319, 1996
A;Title: Developmental and growth temperature regulation of two different mi
A;Reference number: Z16095; MUID:96151506; PMID:8587990
A;Accession: T07688
A;Accession: T07688
A;Accession: T07688
A;Residues: 1-383 <HEP>
A;Residues: 1-383 <HEP>
A;Cross-references: UNIPAC:P48631; UNIPARC:UPI0000033AA2; EMBL:L43921; NID:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 ERAPIDPAPFSLSDLKKAIPAHCFRRSAVWSSCYVVQDLIITFLLYTVANTYIPHLPPPL
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                                                                                                                                                                                                                                                                                                                                                           Query Match
59.4%; Score 1240; DB 2;
Best Local Similarity 57.1%; Pred. No. 1.1e-96;
Matches 206; Conservative 75; Mismatches 78;
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A;Cross-references: UNIPROT:Q41131; UNIPARC:UPI0000033AA5; EMBL:U22378; NID:g722350; PIDP A;Experimental source: strain Baker 296; tissue-type developing endosperm C;Superfamily: fatty acid (acyl-CoA) desaturase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oleate 12-hydroxylase - castor bean
C;Species: Ricinus communis (castor bean)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                        76 VYLAMPVYWFCQSCILIGLWVLGHECGHHAFSEYQWIDNAVGFVLHSALLIPYFSWKYSH
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                     A;Description: desaturates oleic acid to linoleic acid
C;Superfamily: fatty acid (acyl-CoA) desaturase
C;Keywords: oxidoreductase; unsaturated fatty acid biosynthesis
                                                                                                                                                                               84; Indels
                                                                                                                           57.7%; Score 1203; DB 2; 56.0%; Pred. No. 1.4e-93; ive 72; Mismatches 84;
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A,Molecule type: mRNA
                                                                                                                           Query Match
Best Local Similarity 56.0<sup>1</sup>
Matches 204; Conservative
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A;Molecule type: mRNA
A;Residues: 1-378 <HON>
A;Residues: U91341; NID:G2290403;
A;Cross-references: UNIPROT:O24499; UNIPARC:UPI0000037A46; EMBL:U91341; NID:G2290403;
                                                                                                                                                                         Omega-6 desaturase - upland cotton
C;Species: Gossypium hirsutum (upland cotton)
C;Species: Gossypium hirsutum (upland cotton)
C;Daccession: T09880
R;Liu, Q.
R;Liu, Q
LPPYIPHYHAKEASEAIKPILGDYRMIDRTPFFKAMWREAKECIYIEQDADSKHKGTYWY 375
                           77 YLAWPVYWFCQSCILTGLWVLGHECGHHAFSEYQWIDNAVGFVLHSALLTPYFSWKYSHR 136
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Deltal2 fatty acid desaturase (EC 1.14.99.-) [imported] - common sunflower C;Species: Helianthus annuus (common sunflower)
C;Date. 20.5ep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14269
R;Hongtrakul, V.; Slabaugh, M.B.; Knapp, S.J.
submitted to the EMBL Data Library, February 1997
A;Description: Sunflower delta-12 oleate desaturase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RVPIEKPPFTLGOIKOAIPPHCFRRSLLRSFSYVVHDLCLASFFYYIATSYFHFLPOPFS
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nes 205; Conservative
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A;Accession: T14269
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A; Reference number: Z16095; MUID:96151506; PMID:8587990
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Molecule type: mRNA
Residues 1-33 «XIR»
(Cross-references: UNIPROT:024472; UNIPARC:UPI00000A7AA9; EMBL:U86374; NID:g2501791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      omega-6 desaturase FAD2-1, microsomal - soybean
C;Species: Glycine max (soybean)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C;Accession: T07687
R;Heppard, E.P.; Kinney, A.J.; Stecca, K.L.; Miao, G.H.
Plant Physiol: 110, 311-319, 1996
A;Title: Developmental and growth temperature regulation of two different microsomal
                                                                                                                                                                                                                                                                                                                                 acid
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                                                                                                                     LPPYIPHYHAKEASEAIKPILGDYRMIDRTPFFKAMWREAKECIYIEQDADSKHKGTYWY 375
                                                                                                                                    fungal elicitor-induced protein - paraley
C;Species: Petroselinum crispum (paraley)
C;Species: 20-89p-1999 #sequence_revision 20-8ep-1999 #text_change 09-Jul-2004
C;Accession: Tiso43
R;Kirsch, C; Hahlbrock, K; Somssich, I.E.
Plant Physiol. 115, 283-289, 1997
A;Title: Rapid and transient induction of a paraley microsomal delta 12 fatty
A;Reference number: Z18274; MUID:97451781; PMID:9306702
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56.4%; Score 1176; DB 2;
Best Local Similarity 54.5%; Pred. No. 2.7e-91;
Matches 205; Conservative 74; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Cross-references: UNITRAL: C. C. Genetics:
C,Genetics:
A,Gene: BLI12
C,Superfamily: fatty acid (acyl-CoA) desaturase
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C;Species: Lycopersicon esculentum (tomato)
C;Species: Lycopersicon esculentum (tomato)
C;Species: Lycopersicon esculentum (tomato)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
R;Gadea, J.; Mayda, E.; Conejero, V.; Vera, P.
Mol. Plant Microbe Interact: 9, 409-415, 1996
A;Title: Characterization of defense-related genes ectopically expressed in viroid-infect A;Reference number: Z15859; MUID:9625200; PMID:8672818
A;Reference number: Z15859; MUID:9625200; PMID:9672818
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A;Molecule type: mRNA
A;Realdues: 1-33 <GAPA;AB3 delta: UNIPROT:043500; UNIPARC:UPI00000A4D15; EMBL:X94944; NID:g1161567; A;Experimental source: cultivar Rutgers; leaf
                                                                                                             EMBL: L43920; NID: 9904151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 RVPNTKPPFTVGQLKKAIPPHCFQRSLLTSFSYVVVDLSFAFIFY-IATTYFHLLPQPFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 ERAPIDPAPFSLSDLKKAIPAHCFRRSAVWSSCYVVQDLIITFLLYTVANTYIPHLPPPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 RAPIDPAPFSLSDLKKAIPAHCFRRSAVWSSCYVVQDLIITFLLYTVANTYIPHLPPPLV
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                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                              Length 387;
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                                                                                                                                                                                                                                                                                                                                                   Query Match 56.1%; Score 1170.5; DB 2; Length Best Local Similarity 54.0%; Pred. No. 7.9e-91; Matches 194; Conservative 71; Mismatches 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64; Indels
                                                               Query Match 52.3%; Score 1090; DB 2; Best Local Similarity 52.5%; Pred. No. 3.9e-84; Matches 189; Conservative 55; Mismatches 64;
A;Accession: T07687
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fatty acid (acyl-CoA) desaturase
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Avacus mega-3 fatty acid desaturase [imported] - Nostoc sp. (strain PCC 7120)
C,Species: Nostoc sp. PCC 7120
A,Note: Nostoc sp. PCC 7120
A,Note: Nostoc sp. etrain PCC 7120
C,Species: Nostoc sp. etrain PCC 7120
C,Date: Nostoc sp. strain PCC 7120
C,Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 05-Oct-2004
C,Accession: AG2005
R,Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
NARazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak A,Tatle: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anak A,Accession: AG2005
A,Accession: AG2005
A,Accession: AG2005
A,Status: Dreliminary
A,Molecule type: DNA
A,Status: 1-359 exUR>
A,Status: Dreliminary
A,Status: J-359 exUR>
A,Status: J-359 exUR>
A,Status: J-359 exUR>
A,Status: Dreliminary
A,Coose-references: UNIRROT:QBYWL1; UNIRARC:UPI0000CE141; GB:BA000019; PIDN:BAB77963.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hamada, T.; Nishiuchi, T.; Kodama, H.; Nishimura, M.; Iba, K.

Lant Cell Physiol. 37, 606-611, 1996

Lant Cell Physiol. 37, 606-611, 1996

Fittle: CDNA cloning of a wounding-inducible gene encoding a plastid omega-3 fatty acid
Reference number: Z14828; MUID:96416425; PMID:8819308

Accession: T03029
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C;Species: Nicotiana tabacum (common tobacco)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 PFTLQDLKAAIPAECFQPNVSKSLFYFFRDVLIVGLLYAVAH-YLDS-----WYFWPIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 WFCQSCILTGLWVLGHECGHHAFSEYQWIDNAVGFVLHSALLTPYFSWKYSHRKHHANTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLENEEVYIPRIQSQLRTYSTYEFLDNTPGRILLILVIMLTLGFPLYLLTNVSGKKYDRFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NHFDPLSPIFTERERIQVALSDLGIVAVFYGLKFLVQTKGFGWVMCMYGVPVIGLNSFII
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36.1%; Pred. No. 3.2e-46;
ive 74; Mismatches 122; Indels
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NLLKATEAIKPVMGEYYRKSEEPIWKSLWRSCVSCHFV 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: T03029
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-441 <HAM>
A;Cross-references: UNIPROT:P93350; UNIPARC:UPI00000
A;Experimental source: cultivar SR1
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C;Superfamily: fatty acid (acyl-CoA) desaturase
C;Keywords: oxidoreductase
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Matches 122; Conservative
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N;Alternate names: acyl-CoA desaturase; delta12 stearcyl-CoA desaturase; delta9-desatura
C;Species: Chlorella vulgaris
C;Species: Chlorella vulgaris
C;Dates:09-Dec-2002 #sequence_revision 09-Dec-2002 #text_change 09-Jul-2004
C;Accession: JC7871
R;Suga, K.; Honjoh, K.; Furuya, N.; Shimizu, H.; Nishi, K.; Shinohara, F.; Hirabaru, Y.;
Biocci. Biotechnol. Biochem. 66, 1314-1327, 2002
A;Title: Two low-temperature-inducible Chlorella genes for delta12 and omega-3 fatty acis cerevisiae, and expression of omega-3 fad in Nicotiana tabacum.
A;Reference number: JC7871
A;Acession: JC7871
A;Acession: JC7871
A;Acession: JC7871
A;Acession: JC7871
A;Accession: JC7871
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                                                                                                                                                                                                 GKKYDRFTNHFDPLSPIFTERERIQVALSDLGIVAVFYGLKFLVQTKGFGWVMCMYGVPV 255
                                                                                                                                                                                                                                                                                                                315
                                                                                                                                                                                                                                                                                                                                                 214 -GLAGFIVLITLMHTHSSLPHYDSSEMDHLRGALATVDRDYGLLNKVFHNVTDTHVLHH 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 V--YLA-WPVYWFCQSCILTGLWVLGHECGHHAFSEYQWIDNAVGFVLHSALLTPYFSWK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 YSHRKHHANTNSLENEEVYIPRTQSQLRTYSTYEFLDNTPGRILILVIMLTLGFPLYLLT 192
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45.8%; Pred. No. 1e-68;
ive 76; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Superfamily: fatty acid (acyl-CoA) desaturase
                                                                                                                     168; Conservative
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C,Superfamily: fatty acid
C,Keywords: oxidoreductase
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Best Local Similarity
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C;Species: Petrosellinum crispum (paraley)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15039
R;Kirsch, C:; Takamiya-Wik, M.; Reinold, S.; Hahlbrock, K.; Somssich, I.E.
Proc. Natl. Acad. Sci. U.S.A. 94, 2079-2084, 1997
A;Title: Rapid, translent, and highly localized induction of plastidial omega-3 fatty
A;Reference number: 218273; MUID:97203190; PMID:9050908
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-438 «KIR»
A;Residues: 1-438 «KIR»
A;Cross-references: UNIPROT: P933452; UNIPARC: UPI00000A57CA; EMBL:U75745; NID:91786065;
286 GPLQVLKLYGIPYWGFVMWLDIVTYLHHHGHEDKVPWYRGEEWSYLRGGLTTLDRDYGWI 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 LPPPLVYLAWPVYWFCQSCILTGLWVLGHECGHHAFSEYQWIDNAVGFVLHSALLTPYFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DVTHTHVLHHLFPYIPHYHAKBASEAIKPILGDY----RMIDRTPF--FKAMWRBAKECI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 MDERAPIDPA---PFSLSDLKKAIPAHCFRRSAVWSSCYVVQDLIITFLLYTVANTYIPH
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                                                                                                                                                                                                                                                                                                                                                                                               omega-3 fatty acid desaturase (EC 1.14.99.-), chloroplast - parsley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 438;
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29.4%; Score 612.5; DB 2; Length
Best Local Similarity 35.1%; Pred. No. 8.2e-44;
Matches 129; Conservative 70; Mismatches 133; Indels
                                                                                                                                           346 NNIHHDI-GTHVIHHLFPQIPHYHLVEATEAAKPVLGKY 383
                                                                                          NRVFHDVTHTHVLHHLFPYIPHYHAKEASEAIKPILGDY 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Pathway: fatty acid biosynthesis
A;Note: involved in pathogen defense response
C;Superfamily: fatty acid (acyl-CoA) desaturase
C;Keywords: chloxoplast; oxidoreductase
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Job time : 43 secs
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FVSDTGD 423
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Algerence number: 216092
Algerence number: 216092
Algerence number: 216092
Algerens: 107685
Algerens: preliminary: translated from GB/EMBL/DDBJ
Almolecule type: mRNA
Algerences: 1-431 < LEDO.
Algerences: UNIPROT: OB2068; UNIPARC: UPI000009E6DD; EMBL: AJ007739; PIDN: CAA07638.
Algerences: UNIPROT: OBsiree
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                                                                                                                                                                                                                                                                                                                                                                                                                                                142 VWPLYWFAQSTMFWALFVLGHDCGHGSFSNNHKLNSVVGHILHSSILVPYHGWRISHRTH 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139 HANTNSLENEEVYIPRTQSQLRTYSTYEFLDNTPGRILILVIMLTLGFPLYLLTNVSGKK 198
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NyAlternate names: w-3 desaturase
C;Species: Solanum tuberosum (potato)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C;Accession: T07685
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                                                                                                                                                                                                                            PIDPAPFSLSDLKKAIPAHCFRRSAVWSSCYVVQDLIITFLLYTVANTYIPHLPPPLVYL
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                                                                                                                                       32;
                                                 Length 441;
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                                                 Query Match
30.64; Score 638; DB 2; Length 441
Best Local Similarity 37.94; Pred. No. 5.9e-46;
Matches 136; Conservative 62; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
30.4%; Score 634; DB 2; Length 43:
Best Local Similarity 38.9%; Pred. No. 1.3e-45;
Matches 132; Conservative 60; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Pathway: fatty acid biosynthesis
C, Superfamily: fatty acid (acyl-CoA) desaturase
C, Kaywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   314
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GenCore version 5.1.9
(c) 1993 - 2006 Biocceleration Ltd.
                                                                                                       OM protein - protein search, using sw model
                         Copyright
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Run on:

September 22, 2006, 19:35:06; Search time 300 Seconds (without alignments) 1165.520 Million cell updates/sec

2086 1 MSDSYDDRMKDHDMDERAPI.....IYIEQDADSKHKGTYWYHKM 378 US-10-622-774-2

Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2849598 seqs, 925015592 residues Searched:

2849598 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt\_7.2:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

tion	stokesia la	helianthus	calendula o	crepis pala	crepis alpi	dimorphothe	helichrysum	rudbeckia h	vernonia ga	vernonia ga	borago offi	nicotiana t	jatropha cu		crepis pala		vernicia fo	tropaeolum	spinacia ol	hevea brasi	olea europa	sesamum ind	helianthus	punica gran	persea amer	glycine max	cucurbita p	calendula o	linum usita	petroselinu
Description	0689e1	Q7xa13	Q9BCG2		081931		Q7xa08	Q7xa10	Q9sp28	Q9sp29	082729	06dmg8	Q2vg85	041305	065772	084mb7	Q8gzc3	Q583x7	Q8h943	Q461q1	Q4qwz0	091117	Q8w2e9	Q84vt2	Q8h2c3	05£b99	9mnb90	Q9at72	Q38j£7	024471
OI	O6S9E1 STOLA	Q7XA13 HELAN	O9SCG2_CALOF	065771_9ASTR	FAD12 CREAL	Q7XA09 9ASTR	Q7XA08 9ASTR	Q7XA10_RUDHI	Q9SP28_VERGA	Q9SP29_VERGA	O82729_BOROF	Q6DMQ8_TOBAC	Q2VG85 9ROSI	Q41305_SOLCO	O65772 9ASTR	Q84UB7_PUNGR	Q8GZC3_VERFO	Q5S3X7_TROMA	Q8H943 SPIOL	Q461Q1 HEVBR	Q4QWZ0 OLEEU	O9LLL7_SESIN	Q8W2E9 HELAN	Q84VT2 PUNGR	Q8H2C3_PERAE	Q5FB99_SOYBN	Q6QUM6_CUCPE	Q9AT72 CALOF	ı	024471_PETCR
DB	7	7	~	~	Н	7	~	~	~	~	~	~	~	~	N	~	~	~	~	7	7	~	7	~					~	c
Length	378	377	377	374	375	326	326	326	383	383	383	383	383	383	379	387	383	383	382	383	383	383	382	387	382	383.	383	383	378	382
% Query Match	100.0	73.7	73.0	71.6	68.3	67.6	65.6		61.9	61.6	61.3	61.1	61.1	6.09	60.8	9.09	9.09	60.5	60.4	60.4	60.4	60.3	60.2	60.2	0	59.9	9	9	59.4	4
Score	2086	1537.5	1523.5	1493	1424.5	1410	1369	1351	1290.5	1284.5	1279	1274	1274	1271	1268.5	1265	1264	1261	1260	1260	1260	1258	1255.5	1255	1252.5	1250	1250	1242.5	1240	1240
Result No.	1	7	е	4	Ŋ	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53	2

Q8gvc9 olea europa	P48631 glycine max	O81364 prunus arme	O23956 gossypium h	Q8w2b9 gossypium h	09zpi2 brassica ca	Q4pnj0 arachis hyp	Q91kk5 arachis dur	P46313 arabidopsis	O23955 gossypium h	022628 arachis hyp	Q81pe8 brassica ca	Q4u126 arachis hyp	Q9fv88 petroselinu
Q8GVC9_OLEEU	FD6E2 SOYBN	081364 PRUAR	O23956_GOSHI	Q8W2B9_GOSHI	Q9ZPI2 9BRAS	Q4PNJ0_ARAHY	Q9LKK5 9FABA	FADGE ARATH	023955 GOSHI	O22628 ARAHY	Q8LPE8_BRACM	Q4U126 ARAHY	Q9FV88_PETCR
7	-	7	7	~	~	~	~	_	~	~	~	~	7
383	383	346	383	384	384	379	379	383	385	379	384	379	384
59.3	59.2	59.0	58.8	58.5	58.3	58.3	58.3	58.2	58.2	58.2	58.0	58.0	58.0
1238	1234	1230.5	1226	1219.5	1216.5	1216	1216	1215	1214.5	1214	1210.5	1210	1209
32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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61 YTVANTYIPHLPPPLVYLAMPVYWFCQSCILTGLWVLGHECGHHAFSEYQWIDNAVGFVL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 HSALLTPYFSWKYSHRKHHANTNSLENEEVYIPRTQSQLRTYSTYEFLDNTPGRILILVI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                             . .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSDSYDDRAKKOHDMDERAPIDPAPFSLSDLKKAIPAHCFRRSAVWSSCYVVQDLIITFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSDSYDDRMKDHDMDERAPIDPAPFSLSDLKKAIPAHCFRRSAVWSSCYVVQDLIITFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                            Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; campanulids; Asterales; Asteraceae; Cichorioideae; Vernonieae; Stokesia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 378;
                                                                                                                                                                                                                                                                                                                                       EMBL, AY462108; AAR23815.1; -; mRNA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:00160217; F:oxidoreductase activity, acting on paired of GO; GO:0016717; F:oxidoreductase activity, acting on paired of GO; GO:0006633; P:fatty acid biosynthesis; IEA.
InterPro; PR012261; Pacyl Acid desaturation; IEA.
InterPro; IPR012261; Pacyl CoA des.
InterPro; IPR012267; FA_desat_sub.
Propo; PR010257; FA_desat_sub.
Propo; PR08701947; FA_desat_sub.
ProDom; PD001081; FA_desat_sub; 1.
          )
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                                                                                                                                                                                                                                               Hatanaka T., Hildebrand D.F.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        378 AA; 44164 MW; 4DE2346FDB19BE3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 2086; DB 2;
100.0%; Pred. No. 2e-167;
ive 0; Mismatches 0;
                                                05-JUL-2004, integrated into UniProtKB/TrEMBL
                  378 AA.
                  PRT;
                                                               05-JUL-2004, sequence version 1.
OFFEB-2006, entry version 12.
Delta 12 fatty acid epoxygenase.
Stokesia laevis (Stokes aster).
                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 378; Conservative
                                                                                                                                                                                                                 [1] TANCLEOTIDE SEQUENCE.
                                                                                                                                                                                             NCBI_TaxID=13696;
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               QESSEL_STOLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGFPLYLLTNVSGKKYDRFTNHFDPLSPIFTERERIQVALSDLGIVAVFYGLKFLVQTKG 243
                                        FGWVMCMYGVPVIGLNSFIIVITYLHHTHLSSPHYDSTEWNWIKGALTTIDRDFGLLNRV 303
                                                                                                                        PHDVTHTHVLHHLFPYIPHYHAKEASEAIKPILGDYRMIDRTPFFKAMWREAKECIYIEQ 363
                                                                                                                                             183 LGFPLYLLTNISGKKYGRFANHFDPLSPIFTERERIQVVISDIGILAVLYATKLLVEAKG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 RMSDPSEGKNILERVPVDP-PFTLSDLKKAIPTHCFERSVIRSSYXVVHDLIVAYVFYYL
                                                               8 RMKD----HDMDERAPIDPAPFSLSDLKKAIPAHCFRRSAVWSSCYVVQDLIITFLLYTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 ANTYIPHLPPPLUYLAWPUYWFCQSCILTGLWVLGHECGHHAFSEYQWIDNAVGFVLHSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 LLTPYFSWKYSHRKHHANTNSLENEEVYIPRTQSQLRTYSTYEFLDNTPGRILLILVIMLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Developing seed;
MEDLINE=20086417; PubMed=10622705; DOI=10.1016/S0014-5793(99)01541-0;
Fritsche K., Hornung E., Peitzsch N., Renz A., Feussner I.;
"Hoolation and characterization of a calendic acid producing (8,11)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Calendula officinalis (Pot marigold).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
asterids, campanulids, Asterales, Asteraceae, Asteroideae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.0%; Score 1523.5; DB 2; Length 377; 71.7%; Pred. No. 6.2e-120; ive 45; Mismatches 54; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         on paired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         377 AA; 43615 MW; 1CBF7650955F26BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AJ245938; CAB64256.1; -; mRNA.
GO; GO:0016020; C:membrane; IRA.
GO; GO:0016491; P:oxidoreductase activity; IEA.
GO; GO:0016717; F:oxidoreductase activity, acting GO; GO:0016717; F:oxidoreductase activity, acting InterPro; IPR005804; Pa desat.
InterPro; IPR010257; FA_desat_sub.
Projom; PD001081; FA_desat_sub.
Projom; PD001081; FA_desat_sub; 1.
                                                                                                                                                                                                                                                                                                                                                 QSCG2_CALOF PRELIMINARY, PRT; 377 AA. Q9SCG2, CALOF PRELIMINARY, PRT; 377 AA. Q9SCG2, LAKY-2000, integrated into UniProtKB/TrEMBL. 01-MAY-2000, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  07-FEB-2006, entry version 20. (8,11)-linoleoyl desaturase (Fragment).
                                                                                                                                                                                                        DADSKHKGTYWYHKM 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linoleoyl desaturase.";
FEBS Lett. 462:249-253(1999)
                                                                                                                                                                                                                               DEDSEHKGTYWYHKM
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    MLTLGFPLYLLTNVSGKKYDRFTNHFDPLSPIFTERERIQVALSDLGIVAVFYGLKFLVQ 240
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GO; GO:0016020; C:membrane; I:mRNA.

GO; GO:0016717; F:oxidoreductase activity, acting on paired d. .; IEA.

GO; GO:0016633; P:fatty acid biosynthesis; IEA.

GO; GO:0006633; P:fatty acid biosynthesis; IEA.

Interbro; IRR012261; Fa acil-CoA des.

Interbro; IRR012061; Fa desat.

Interbro; IPR010257; FA desat.

Pfam; PF00487; FA desaturase; I.

PRSF; PIRSF000347; FA acyl-CoA des; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                     241 TKGFGWVMCMYGVPVIGLNSPIIVITYLHHTHLSSPHYDSTEWNMIKGALTTIDRDFGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGFPLYLLTNVSGKKYDRFTNHFDPLSPIFTBRERIQVALSDLGIVAVFYGLKFLVQTKG
                                                                                                                            NRVFHDVTHTHVLHHLFPYIPHYHAKEASEAIKPILGDYRMIDRTPFFKAMWREAKECIY
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                                                                                                                                                                                                                                                                                                                                                                                       01-007-2003, integrated into UniProtkB/TrEMBL.
01-007-2003, sequence version 1.
01-007-2005, entry varsion 14.
Deltal2-fatty acid acetylenase.
Helianthus annus (Common sunflower).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; esterids; campanulids; Asteraceae; Asteroideae; Heliantheae; Helianthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLECTIDE SEQUENCE.

NUCLECTIDE SEQUENCE.

MEDLINE-22674157; PubMed=1278757.x;

MODI=10.1046/j.1365-213X.2003.01757.x;

Cahoon R.B., Schnurr J.A., Huffman E.A., Minto R.E.;

evolutionarily distant plant families.";

Plant J. 34:671-683(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73.7%; Score 1537.5; DB 2; Length
72.8%; Pred. No. 4e-121;
ive 41; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             377 AA; 43751 MW; 832C8A129C6C2A55 CRC64;
                                                                                                                                                                                                                                                                                                                                                      377 A.A.
                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                 361 IEQDADSKHKGTYWYHKM 378
                                                                                                                                                                                                            IEQDADSKHKGTYWYHKM 378
                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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Q7xa13;
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                                                                                                                                                                                                           246 ACMYGVPVLGVFTFFDVITFLHHTHQSSPHYDSTEWNWIRGALSAIDRDFGFLNSVFHDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Green A., Stymne S.;
"Identification of non-heme diiron proteins that catalyze triple bond and epoxy group formation.";
Science 280:915-918(1998).
-!- FUNCTION: Changes the delta-12 double bond of linoleic acid into a triple bond in the bionymthesis of crepenynic acid.
-!- CATALYTIC ACTIVITY: Linoleate + AH(2) + O(2) = crepenynate + A +
                                                                             LYLLTINVSGKKYDRFTNHFDPLSPIFTERERIQVALSDLGIVAVFYGLKFLVQTKGFGWV
                                                                                                          248 MCMYGVPVIGLNSFIIVITYLHHTHLSSPHYDSTEWNWIKGALTTIDRDFGLLNRVFHDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [MRNA].
MEDLINE=98239771; PubMed=9572738; DOI=10.1126/science.280.5365.915;
Lee M., Lenman M., Banas A., Bafor M., Singh S., Schweizer M.,
Nilsson R., Liljenberg C., Dahlqvist A., Gummeson P.O., Sjoedahl S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Crepis alpina.
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, asterids, campanulids, Asterales, Asteraceae, Cichorioideae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-WAR-2001, sequence version 2.
07-FBB-2006, entry version 43.
Delts (12) fatry acid dehydrogenase (BC 1.14.99.33) (Crepenynate synthase) (Delta-12 fatry acid acetylenase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- PATHWAY: Polyunsaturated fatty acid biosynthesis.
-i- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- DOMAIN: The histidine box domains may contain the active and/or be involved in metal ion binding.
-!- SIMILARITY: Belongs to the fatty acid desaturase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00487; FA desaturase; 1.
PIRSF; PIRSF000347; FA acyl-CoA des; 1.
PIRSF PD001081; FA desatusub; 1.
Fatty acid biosynthesis; Iron; Lipid synthesis; Membrane; Oxidoreductase; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-OCT-2001, integrated into UniProtKB/Swiss-Prot.
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InterPro; IPR012261; FA acyl-CoA_des.
InterPro; IPR05804; FA desat.
InterPro; IPR010257; FA_desat_sub.
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-!- TISSUE SPECIFICITY: Seed.
                                                                                                                                                                                                                                                                                                                                                                                           KHKGTYWYHKM 378
                                                                                                                                                                                                                                                                                                                                                                                                                                           364 KLKGVYWYHKL 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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NCBI_TaxID=72610;
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TRANSMEM
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081931;
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P1479
P1474
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                                                                                243 AAWVINMYAIPVLGVSVFFVLITYLHHTHLSLPHYDSTEWNWIKGALSTIDRDFGFLNRV 302
                                                                                                                                                                                     303 FHDVTHTHVLHHLISYIPHYHAKEARDAIKPVLGEYYKIDRTPIFKAMYREAKECIYIEP 362
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        LGFPLYLLTNISGKKYGRFANHFDPMSPIFNDRERVQVLLSDFGLLAVFYAIKLLVAAKG 242
                                                                                                                                                          PHDVTHTHVLHHLFPYIPHYHAKEASEAIKPILGDYRMIDRTPFFKAMWREAKECIYIEQ 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . .; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLIRE=98239771; PubMed=9572738; DOI=10.1126/science.280.5365.915; Lee M., Lenman M., Banas A., Bafor M., Singh S., Schweizer M., Nilsson R., Liljenberg C., Dahlqvist A., Gummeson P.O., Sjoedahl S., Green A., Stymme S.; "Identification of non-heme diiron proteins that catalyze triple bond and epoxy group formation."; Science 280:915-918(1998).
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                                                        FGWVMCMYGVPVIGLNSFIIVITYLHHTHLSSPHYDSTEWNWIKGALTTIDRDFGLLNRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1998, integrated into UniProtKB/TrEMBL.
01-AUG-1998, sequence version 1.
07-FEB-2006, entry version 29.
Delta 12 fatty acid epoxygenase.
Crepis palaestina.
Everyis palaestina.
Spermatophyta, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons; asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0016020; C:membrane; IEA.

GO; GO:0016017; F:oxidoreductase activity, acting on paired d.

GO; GO:0006633; P:fatty acid biosynthesis; IEA.

GO; GO:0006636; P:fatty acid desaturation; IEA.

InterPro; IPR012261; FA acyl-CoA des.

InterPro; IPR010257; FA desat.

InterPro; IPR010257; FA desat.

Pfam; PF00487; FA desaturase; 1.

PIRSF; PIRSF000347; FA acyl-CoA des; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                DADSKHKGTYWYHKM 378
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DEDSEHKGVFWYHKM 377
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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NCBI_TaxID=72611;
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Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                239 THLSLPHYDSSEWNWIKGALSTIDRDFGFLMRVFHDVTHTHVLHHLISYIPHYAKBARD
                                                                                                                                                                                                                                              LIGLWVLGHECGHHAFSEYQWIDNAVGFVLHSALLTPYFSWKYSHRKHHANTNSLENEEV
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07-FEB-2006, entry version 12.
Deltal2-fatty acid acetylenase (Fragment).
Helichryum bracteatum.
Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta, agermatophyta, aganoliophyta, edicotyledons; core eudicotyledons; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Gnaphalieae; Helichrysum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AX166778; AA038037.1; -; Genomic_DNA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0016491; F:oxidoreductase activity; IEA.

GO; GO:001671; F:oxidoreductase activity, acting on paired d.

GO; GO:0006636; P:fatty acid desaturation; IEA.

InterPro; IPR0005804; Fa_desat.

InterPro; IPR010257; FA_desat.

Probom; PP001081; FA_desaturase; 1.

Probom; PD001081; FA_desat_sub; 1.
                                                                                                                                                           5.
                                                                                                                               Length 326;
                                                                                                                            tch 67.6%; Score 1410; DB 2; Length 3 al Similarity 75.9%; Pred. No. 2e-110; 249; Conservative 32; Mismatches 45; Indels
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DOI=10.1046/j.1365-313X.2003.01757.x;
Cahoon B.B., Schnurr J.A., Huffman B.A., Minto R.E.;
"Fungal responsive fatty acid acetylenases occur widely evolutionarily distant plant families.";
Plant J. 34:671-683(2003).
                                                                                                    37813 MW; 9787D6D1444EA3E0 CRC64;
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InterPro; IPR010257; FA desat sub.
Pfam; PF00487; FA desaturase; 1.
ProDom; PD001081; FA desat_sub; 1.
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NCBI_TaxID=220345;
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GO, GO:0016020; C:membrane; IEA.
GO, GO:0016491; F:oxidoreductase activity; IEA.
GO, GO:00164717; F:oxidoreductase activity, acting on paired d. . .; IEA.
GO, GO:0006636; P:fatty acid desaturation; IEA.
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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                        RMKDHDMDERAPI DPAPFSLSDLKKAI PAHCFRRSAVWSSCYVVQDLI ITFLLYTVANTY
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01-OCT-2006, entry version 11.
Delta12-fatty acid acetylenase (Fragment).
Dimorphochaca sinuata (African daisy).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, agermatophyta, adaloliophyta, eddicotyledons, astarids; campanulids, Asterales, Asteraceae; Asteroideae; Calenduleae, Dimorphotheca.
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                                                                                                                                  DB 1; Length 375;
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MUCLEOLINE=22674157; PubMed=12<sup>8</sup>87248;
DOI=10.1046/j.1365-313X.2003.01757.x;
Cahoon E.B., Schnurr J.A., Huffman E.A., Minto R.E.;
"Fungal responsive fatty acid acetylenases occur widely evolutionarily distant plant families.";
Plant J. 34:671-683(2003).
                Potential.
Potential.
Potential.
Histidine box-1.
Histidine box-2.
Histidine box-3.
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; Pred. No. 1.4e-111
55; Mismatches 68
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Q7XA09_9ASTR PRELIMINARY; PRT;
Q7XA09;
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Best Local Similarity 65.9%;
Matches 244; Conservative 55
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01-OCT-2003, sequence version 1.
01-OCT-2006, entry version 1.
07-FBB-2006, entry version 13.
Delta12-fatty acid acetylenase (Fragment).
Rudbeckia hirta (Black-eyed Susan).
Rudbeckia hirta (Black-eyed Susan).
Spermatophyta; Viidiplantee; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; angnoliophyta; eudicotyledons; asterids; campanulids; Asterales, Asteraceae; Asteroideae;
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GO, GO:0016020; C:membrane; IEA.
GO, GO:0016491; F:oxidoreductase activity, acting on paired d.
GO; GO:001671; F:oxidoreductase activity, acting on paired d.
GO; GO:0006636; P:fatty acid desaturation; IEA.
InterPro; IPR005804; Fa desat.
InterPro; IPR01257; FA desat_sub.
Propom; PD001081; FA desat_sub.
                                                                                                  Length 326;
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DOI=10.1046/j.1365-313X.2003.01757.x;
DOI=10.1046/j. Huffman E.A., Minto R.E.;
"Fungal responsive fatty acid acetylenases occur widely in evolutionarily distant plant families.";
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326 AA; 37865 MW; D3C65BAD9EF25783 CRC64;
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326 326
326 AA; 38030 MW; D355816CF4AA2829 CRC64;
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                                                                                                ;; Score 1369; DB 2;
;; Pred. No. 5.7e-107;
32; Mismatches 52;
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73.8%;
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Matches 242; Conservative
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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                KAIPAHCFRRSAVWSSCYVVQDLIITFLLYTVANTYIPHLPPPLVYLAWPVYWFCQSCIL
                                                         Gaps
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R GO; GO:0016020; C:membrane; IEA.

R GO; GO:0016020; C:membrane; IEA.

R GO; GO:0016717; F:oxidoreductase activity, acting on paired d...

R GO; GO:0006631; P:phosphatidylcholine desaturase activity; IEA.

R GO; GO:0006631; P:fatty acid biosynthedis; IEA.

R GO; GO:0006631; P:fatty acid desaturation; IEA.

R InterPro; IPR012561; FA_Gesat.

R InterPro; IPR010257; FA_Gesat.

R PIRSF; PIRSF000347; FA_Gesat.

R PIRSF; PIRSF000347; FA_Gesat.

R Probom; PD001081; FA_Gesat.

R Probom; PD001081; FA_Gesat.

R Oxidoreductase.
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PubMed=10759541;

Hage T.G., Seither C., Hildebrand D.;

Hisolation of two cDNAs from Vernonia galamensis (Cass.) Less.

encoding a microsomal oleate desaturase (FAD2) (accession nos.

encoding a and API88264) and functional expression in Saccharomyces

cerevisiae (PGR00-035)...;

Plant Physiol. 122:1457-1457 (2000).
                                                      5;
                                                      Indels
Length
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                                                         52;
64.8%; Score 1351; DB 2; 72.3%; Pred. No. 1.9e-105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000, integrated into UniProtKB/TrEMBL 01-MAY-2000, sequence version 1. 07-FBB-2006, entry version 24.
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                                                         37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             332 IKPILGDYRMIDRTPFFKAMWREAKECI 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               299 IKPVLGEFYKIDRTPIFKAMWRXAKEXV 326
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Query Match
Best Local Similarity 72.39
Matches 237; Conservative
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PRT;
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                  44268 MW;
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60.1%;
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                                                                                                Matches 218; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NVK-DGVYWY 379
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                  383 AA;
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SEQUENCE 383
  Oxidoreductase
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O82729;
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                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DVTHTHVLHHLFPYIPHYHAKEASBAIKPILGDYRMIDRTPFFKAMWREAKECIYIEQDA 365
                                                                                65
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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                   FPLYLLTNVSGKKYDRFTNHFDPLSPIFTERERIQVALSDLGIVAVFYGLKFLVQTKGFG
                                                                              DDRMKDHDMDERAPIDPAPFSLSDLKKAIPAHCFRRSAVWSSCYVVQDLIITFLLYTVAN
                                                                                                                                                              TYIPHLPPPLVYLAWPVYWFCQSCILTGLWVLGHECGHHAFSEYQWIDNAVGFVLHSALL
                                                                                                                                                                                                                                            TPYFSWKYSHRKHHANTNSLENEEVYIPRTQSQLRTYSTYEFLDNTPGRILILVIMLTLG
                                                                                                                                                                                                                                                                                                                                                                                                            WVMCMYGVPVIGLNSFIIVITYLHHTHLSSPHYDSTEWNWIKGALTTIDRDFGLLNRVFH
                                        Gaps
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
asterids, campanulids, Asterales, Asteraceae, Cichorioideae;
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NUCLECTIDE SEQUENCE.
NUCLECTIDE SEQUENCE.
Hage T.G., Seither C., Hildebrand D.;
Hage T.G., Seither C., Hildebrand D.;
"Isolation of two cDNAs from Vernonia galamensis (Cass.) Less.
encoding a microsomal oleate desaturase (FAD2) (accession nos.
encoding a microsomal oleate desaturase (FAD2) (accession nos.
AF188263 and AF188264) and functional expression in Saccharomyces
                                        ë,
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GO; GO:0016020; C:membrane; IEA.

GO; GO:0016171; F:oxidoreductae activity, acting on paired d.

GO; GO:001617; F:oxidoreductae activity, acting on paired d.

GO; GO:0006633; P:fatty acid blosynthesis; IEA.

GO; GO:0006633; P:fatty acid blosynthesis; IEA.

InterPro; IPR012261; FA acyl-COA_des.

InterPro; IPR012057; FA desat.

InterPro; IPR010257; FA desat.

Pfam; PF00407; FA desaturase; I.

Pfam; PF00407; FA desaturase; I.

PROMOGO; FA desaturase; I.

PROMOGO; FA desaturase; I.
Length 383;
                                        Indels
  DB 2;
                                          80;
61.9%; Score 1290.5; DB 2
59.2%; Pred. No. 2.9e-100;
iive 68; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000, integrated into UniProtKB/TrEMBL.
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07-FEB-2006, entry version 24.
07-ELB-12 oleate desaturase (EC 1.3.1.35).
Name=FAD2-1;
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Query Match
Best Local Similarity 59.21
Matches 219, Conservative
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                             66 TYIPHLPPPLVYLAMPVYWPCQSCILTGLWVLGHEGGHHAPSEYOMIDNAVGFVLHSALL
                                                                                                                                                                                                                                                                                                                                                                          DVTHTHVLHHLFPYIPHYHAKEASEAIKPILGDYRMIDRTPFFKAMWREAKECIYIEQDA
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                                                                                                                                                DDRWKDHDMDERAPIDPAPFSLSDLKKAIPAHCFRRSAVWSSCYVVQDLIITFLLYTVAN
                                                                                                                                                                                                                                                                                               73 NYIPLLPHPLSYVAWPVYWIFQGCVLTGVWVIAHECGHHAFSDYQWLDDTVGLILHSALL
                                                                                                                                                                                                                                                                                                                                                126 TPYFSWKYSHRKHHANTNSLENEEVYIPRTOSQLRTYSTYEFLDNTPGRILILVIMLTLG
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Borago officinalis (Bourrache) (Borage).

Borago officinalis (Bourrache) (Borage).

Borago officinalis (Bourrache) (Borage).

Subaryora, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, eudicotyledons; core eudicotyledons; asterids; lamiids; Boraginaceae; Borago.
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                                              Length 383;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sayanova O., Shewry P.R., Napier J.A.;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
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C16B93BE7F94DA80 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
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IEA.
                                                 DB 2;
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0016717; F:oxidoreductase activity, acting
GO; GO:0006633; P:fatty acid biosynthesis; IEA.
GO; GO:0006636; P:fatty acid desaturation; IEA.
InterPro; IPR012261; FA_acyl-CoA_des.
InterPro; IPR0102561; FA_desat_sub.
Pfam; PF00487; FA_desat_sub.
Pfam; PF00487; FA_desat_sub.
PINSF; PIRSF000347; FA_acyl-CoA_des; 1.
                                                                           Pred. No, 9.4e-100;
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Pred. No. 2.7e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1998, integrated into UniProtKB/TrEMBL. 01-NOV-1998, sequence version 1. 07-FEB-2006, entry version 26.
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                                              61.6%; Score 1284.5; 58.9%; Pred. No. 9.4e
                                                                                               68; Mismatches
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Gaps

5;

75 8 135

141

195 199 255 315

379

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200 GRHYDRFACHYDPYGPIYNDRERLQIFLSDAGVLGAGYLLYRIALVKGLAWLVCMYGVPL 259
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                                                                                                                                                                                                                                                                                                       136 RKHHANTNSLENEEVYIPRTQSQLRTYSTYEFLDNTPGRILILVIMLTLGFPLYLLTINVS
                                                                                                                                                                                                                                                                                                                                260 LIVNGFLVLITYLQHTHPSLPHYDSSEWDWLRGALATVDRDYGILNKVFHNITDTHVVHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 EKVPTSKPPFTVGDIKKAIPPHCFQRSLVRSFSYVVXDLILVSVFYYIAITYFHLLPSPY
                                                                                                                                                                                                                    76 VYLAWPVYWFCQSCILTGLWVLGHECGHHAFSEYQWIDNAVGFVLHSALLTPYFSWKYSH
                                                                                                                                                                                                                                             GKKYDRFTNHFDPLSPIFTERERIQVALSDLGIVAVFYGLKFLVQTKGFGWVMCMYGVPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    256 IGLNSFIIVITYLHHTHLSSPHYDSTEWNWIKGALTTIDRDFGLLNRVFHDVTHTHVLHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LFPYIPHYHAKEASEAIKPILGDYRMIDRTPFFKAMWREAKECIYIEQDADSKHKGTYWY
                                                                                                                              16 ERAPIDPAPFSLSDLKKAIPAHCFRRSAVWSSCYVVQDLIITFLLYTVANTYIPHLPPPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 383;
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                                                                                   80;
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7D75199984305393
                                    61.1%; Score 1274; DB 2; 58.6%; Pred. No. 7.2e-99;
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10-JAN-2006, sequence version 1.
07-WAR-2006, entry version 4.
Delta12-fatty acid desaturase.
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                                                                                     67; Mismatches
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43933 MW;
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                                                                                     211; Conservative
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NCBI_TaxID=180498;
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Best Local Similarity
383 AA;
                                         Query Match
Best Local Similarity
Matches 211; Conserv
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                                                                                                                                                                                                                                             NVSGKKYDRFTNHFDPLSPIFTERERIQVALSDLGIVAVFYGLKFLVQTKGFGWVMCMYG 252
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                                                                                                                                                                                                                                                                                                                                     VPVIGLNSFIIVITYLHHTHLSSPHYDSTEWNWIKGALTTIDRDFGLLNRVFHDVTHTHV
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                                           DMDERAPIDPAPFSLSDLKKAIPAHCFRRSAVWSSCYVVQDLIITFLLYTVANTYIPHLP
  Gaps
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"FADZ-silencing has pleiotropic effect on polar lipids of larticed effect in different organs of transgenic tobacco.";
Plant Sci. 170:170-177(2006).
  81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Wisconsin 38;
Yang M.F., Zhang F.Y., Zheng G.L., Xu Y.N.;
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
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GO; GO: 0016717; F:oxidoreductase activity, acting on GO; GO: 0006631; P: fatty acid biosynthesis; IEA.
GO; GO: 0006635; P: fatty acid desaturation; IEA.
INTERPRO; IPR012261; FA_acyl-CoA_des.
INTERPRO; IPR012261; FA_desat.
INTERPRO; IPR010297; FA_desat.
INTERPRO; IPR00487; FA_desat.sub.
Pfam; PF00487; FA_desaturase; I.
PIRSF; PIRSF000347; FA_acyl-CoA_des; I.
ProDom; P0010181; FA_desat_sub; I.
Oxidoreductase.
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  Mismatches
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  62;
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  218; Conservative
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NUCLEOTIDE SEQUENCE
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QEDMQ8;
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                                                LFPYIPHYHAKEASEAIKPILGDYRMIDRTPFFKAMMREAKECIYIEQDADSKHKGTYWY 375
260 LVVNGFLVLITYLQHTHPSLPHYDSTEWDWLRGALATCDRDYGVLNKVFHNITDTHVVHH 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
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MEDINE-8923771; PubMed=9572738; DOI=10.1126/science.280.5365.915;
MEDINE-80239771; PubMed=9572738; DoI=10.1126/science.280.5365.915;
MEDINE-8023771; PubMed=9572738; Dafor M., Singh S., Schweizer M.,
Nilsson R., Liljenberg C., Dahlqvist A., Gummeson P.O., Sjoedahl S.,
                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons, asterids, campanulids, Asterales, Asteraceae, Cichorioideae,
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GO; GO:0016020; C:membrane; IEA.

GO; GO:0016717; F:oxidoreductase activity, acting on paired d.

GO; GO:0016633; P:fatty acid biosynthesis; IEA.

GO; GO:0006636; P:fatty acid desaturation; IEA.

InterPro; IPR012261; FA acyl-CoA_des.

InterPro; IPR012261; FA_desat_sub.

InterPro; IPR010257; FA_desat_sub.

Pfam; PF00487; FA_desat_sub.

Pfam; PF00487; FA_desat_sub.

Pfam; PF00487; FA_desat_sub.
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01-AUG-1998, sequence version 1.
07-FBB-2006, entry version 29.
Delta 12 fatty acid desaturase.
Crepis palaestina.
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nes 221; Conservative
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065772;
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                                                                                  256 IGLNSFIIVITYLHHTHLSSPHYDSTEWNWIKGALTTIDRDFGLLNRVFHDVTHTHVLHH 315
                                                                                                                                                                                                                                                   LPPYIPHYHAKEASEAIKPILGDYRMIDRTPFFKAMWREAKECIYIEQDADSKHKGTYWY 375
                                                                                                                                                                                                                                                                               GKKYDRFTNHFDPLSPIFTERERIQVALSDLGIVAVFYGLKFLVQTKGFGWVMCMYGVPV 255
     RRHHSNTGSLERDEVFVPKKKSNIRWFSKY--LNNLPGRLFTLTITLALGWPLYLAFNVS 199
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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLECTIDE SEQUENCE.
Consiglio F., Amatruda M.R., Leone A., Costa A., Grillo S., Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          on paired
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GO; GO: 001617; F: oxidoreductase activity, acting on GO; GO: 0006630; P: fatty acid biosynthesis; IEA.
GO; GO: 0006636; P: fatty acid desaturation; IEA.
InterPro; IPR012261; FA_acyl-CoA_des.
InterPro; IPR015261; FA_desat.
InterPro; IPR015267; FA_desat.
InterPro; IPR016257; FA_desat.
InterPro; IPR01637; FA_desaturase; I.
PIRSF; PIRSF000347; FA_desaturase; I.
PIRSF; PIRSF000347; FA_desat_sub.
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58.3%; Pred. No. 1.
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PIR; T10480; T10480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-FEB-2006, entry version 29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996, integrated into
                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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Matches 210; Conservative
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244 LGWVLAMYGGPLLVVNGFLVLITFLQHTHASLPHYDSTEWDWLRGALATIDRDYGILNKV 303
         8 8 8 8
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304 FHDVTHTHVLHHLFPYIPHYHAKEASEAIKPILGDYRMIDRTPFFKAMWREAKECIYIEQ 363 304 FHNITDTHVTHLESTWPHYHAKEASEAIKFILGDYYOPDGTSGYKANYRETKECIYUDK 363	REAKECIYIEQ 36	:: = =	RETKECIYVDK 36
304 FHDVTHTHVLHHLFPYIPHYHAKEASEAIKPILGDYRU   :-	MIDRIPFFKAMW	= = -	DPDGTSVFKAMY
304 FHDVTHTHVLHHLFPYIPHYHAKEA	SEAIKPILGDYR	= = = ::	TKAIKPILGDYYC
304 FHDVTHTHVLHHI   ::          304 FHNITDTHVTHHI	FPY I PHYHAKEA	= = = -	FSTMPHYHAMEA
304 F	HDVTHTHVLHHL	= = = ::	THNITDTHVTHHL
	304 F		304 F

<sup>364</sup> DADSKHKGTYWY 375 ||:|||||| 364 DAEVK-DGVYWY 374

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Search completed: September 22, 2006, 19:43:23 Job time : 304 secs

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us-10-622-774-1.rst

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September 24, 2006, 23:03:22; Search time 7201 Seconds (without alignments) 10918.286 Million cell updates/sec
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                     OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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90-est3::;

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90-est6::;

90-est7::;

90-est9::;

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Perfect score:
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	ជ្	CLPY8290.	CLPY8434.	CLVY10747	CLPX8050.	CLPY5158.	CLPY5660.	CLPY8633.	CLPY5873.	CLPY4893.	CLPY13180	CLPY14207	CLPY13349	CLPY8961.	CLPY13299	CLPY7316.	CLSX4996.	CLPY2215.	CLPY8440.	CLPY8857.
	Description	DW097268	DW097410	DW158633	DW085008	DW093963	DW094502	DW097606	DW094732	DW093673	DW089055	DW090169	DW089237	DW097931	DW089183	DW096275	DW128132	DW090949	DW097416	DW097829
SUMMARIES	ΩI	DW097268	DW097410	DW158633	DW085008	DW093963	DW094502	DW097606	DW094732	DW093673	DW089055	DW090169	DW089237	DW097931	DW089183	DW096275	DW128132	DW090949	DW097416	DW097829
	DB	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
	% Query Match Length DB	1047	982	941	937	921	922	927	922	906	928	898	893	942	919	908	882	906	906	953
	& Query Match	40.2	36.3	35.8	35.2	35.1	35.1	35.1	35.0	35.0	35.0	34.5	34.4	34.4	34.2	34.2	34.1	34.1	33.8	33.8
	Score	564.6	509.8	503.2	495.4	493.2	493.2	493.2	492.2	491.8	491.6	485.2	483.4	483	481.2	480.8	479.4	479	475.8	475.4
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DW084498 CLPX7530. DW098114 CLPY9145. DW114008 CLPX9045.	,		DW079511 CLPX1629. DW092156 CLPY3452. DW094175 CLPY5354			BQ994479 QGF7F12.Y DW096751 CLPY7762.	DT211274 N107 H01 DW094388 CLPY5554.	DW098230 CLPY9262. DW093011 CLPY4281.	DW087447 CLPY10938 DW048664 CLLX15243	_	DW092317 CLPY3617. DW097877 CLPY8906.
DW084498 DW098114	DW093425 DW084816	DW094062 DW119170 DW084758	DW079511 DW092156	DW091892	DW097104 DW094401	BQ994479 DW096751	DT211274 DW094388	DW098230 DW093011	DW087447 DW048664	DW058651	DW092317 DW097877
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33.7	33.4	33.1 33.0	33.0	32.4	31.9	31.5	31.1	30.9	30.5	29.7	29.6 29.6
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## ALIGNMENTS

RESULT 1	
LOCITS	nw007058 1047 hr mBNA linear RST 22-DRC-2005
DOCOS	b) C10 ab) C1.D(XV2) lettince nerennis Lacting
NOT THE SEC	clone CLPY8290, mRNA sequence.
ACCESSION	DW097268
VERSION	DW097268.1 GI:83895188
KEYWORDS	EST.
SOURCE	Lactuca perennis
ORGANISM	Lactuca perennis
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
	Cichorieae; Lactuca.
REFERENCE	1 (bases 1 to 1047)
AUTHORS	Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
	Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J.,
	Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
	Lai, Z., Church, S., Jackson, L. and Bradford, K.
TITLE	Lettuce and Sunflower ESTs from the Compositae Genome Project
	http://compgenomics.ucdavis.edu/
JOURNAL	Unpublished (2002)
COMMENT	Contact: Alexander Kozik [R.W.Michelmore]
	Department of Vegetable Crops, R.W.Michelmore Lab
	University of California at Davis (UCD)
	Asmundson Hall, UCD, Davis, CA 95616, USA
	Tel: 1-(530)-742-1742
	Fax: 1-(530)-752-9659
	Library was sequenced at Joint Genome Institute, Walnut Creek CA,
	using ABI 3730 machines.
FEATURES	Location/Qualifiers
source	11047
	/organism="Lactuca perennis"
	/mol_type="mRNA"
	/strain="PI-274378"
	/db xref="taxon:43195"
	/clone="CLPY8290"
	/lab host="E.coli"
	d library
	constructed from multiple sources of RNA from a single

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/clone_lb="CLP(XXZ) lettuce perennis"
/note="Vector: pBRcDNASfiAB; The standard library was
/note="Vector: pBRcDNASfiAB; The standard library was
constructed from multiple sources of RNA from a single
genotype. cDNAs were then size-fractionated, directionally
cloned into a custom medium-copy vector and
transformations made with three size classes
(X-large, Y-medium and Z-small) to minimize size bias due
to differential transformation efficiency. Details of
each source of RNA and library construction can be
obtained at http://cgpdb.ucdavis.edu/"
                                                                                                                                                                                                                                                                                                                                                                       982 bp mRNA linear EST 22-DEC-2005
D22.abl CLP(XXZ) lettuce perennis Lactuca perennis CDNA
GTTACACACACCCACGTGTTGCACCATTTGTTTCCCTACATTCCACATTATCATGCAAAG 1069
                                                           Grincacacacacarcarcacarcacarcararacaracacacacararcaracana 1045
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
asterids, campanulids, Asterales, Asteraceae, Cichorioideae,
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1 (bases 1 to 982)
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Elison, P., Kolkman, J., Slabaudi, M.S., Livingston, K., Zhou, Y., Blison, P., Kolkman, J., Slabaudi, M.S., Livingston, K., Zhou, Y., Liai, Z., Church, S., Jackson, L. and Bradford, K. Lettuce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 GATCCATCTAAGGACAACGATATACTAAAACGTGTCCCGGTTGA---GCCACCATTCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Alexander Kozik [R.W.Michelmore]
Contact: Alexander Kozik [R.W.Michelmore Lab
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundaon Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
Library was sequenced at Joint Genome Institute, Walnut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
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75.3%; Pred. No. 1.1e-118;
tive 0; Mismatches 212; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Lactuca perennis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://compgenomics.ucdavis.edu/
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="taxon:43195"
                                                                                                                                                                                                                                                                                                                                                                                                                                             clone CLPY8434, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="PI-274378"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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DW097410.1 GI:83895330
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constructed from multiple sources of RNA from a single
genotype. cDNAs were then size-fractionated, directionally
cloned into a custom medium-copy vector and
transformations made with three size classes
(X-large,Y-medium and Z-small) to minimize size bias due
to differential transformation efficiency. Details of
each source of RNA and library construction can be
obtained at http://cgpdb.ucdavis.edu/"
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        Contact: Alexander Kozik [R. W. Michelmore]
Department of Vegetable Crops, R. W. Michelmore Lab
Department of Vegetable Crops, R. W. Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1. (530) -742-1959
Fax: 1- (530) -752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
Library was sequenced at Joint Genome Institute, Walnut Creek (using ABI 3730 machines.
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                                                                                                                                                                                                                                                   organism="Lactuca virosa"
                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:75947"
                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                         /clone="CLVY10747"
                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="UK-1"
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
asterids, campanulids, Asterales, Asteraceae, Cichorioideae,
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(Cichorieae; Lactuda.

(Dases 1 to 941)

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J.,
Ellison, P., Kolkman, J., Slabaugh, M. S., Livingston, K., Zhou, Y.,
Latiz., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTS from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
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    CAAGCTAGCATTCTTACTGGCTTATGGGTCATCGGTCATGAATGTGGTCACCATGCTTT
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                                                                 TACATTCCTCACCTCCCTCCTCCTCTAGTTTACTTAGCATGGCCGGTTTACTGGTTTTGC
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      Length 937;
Score 495.4; DB 10; Length
Pred. No. 5e-115;
0; Mismatches 199; Indels
   Query Match
Best Local Similarity 75.5%;
Matches 642; Conservative
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/note="Vector: pBRcDNASfiAB; The standard library was
/note="Vector: pBRcDNASfiAB; The standard library was
constructed from multiple sources of RNA from a single
genotype. CDNAs were then size-fractionated, directionally
cloned into a custom medium-copy vector and
transformations made with three size classes
(X-large, Y-medium and Z-small) to minimize size bias due
to differential transformation efficiency. Details of
each source of RNA and library construction can be
obtained at http://cgpdb.ucdavis.edu/"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                937 bp mRNA linear EST 22-DEC-2005 CLPX8050.bl D22.abl CLP(XXZ) lettuce perennis Lactuca perennis cDNA DW085008
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1 (bases 1 to 937)

1 (bases 1 to 937)

1 (bases 1 to 937)

1 Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison, P., Kolkman, D., Chavalier, P., Ziegle, J., Lai, Z., Church, S., Jackson, L. and Bradford, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K., Chou, Y., Lettuce and Sunflower ESTs from the Compositae Genome Project Unpublished (2002)
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Library was sequenced at Joint Genome Institute, Walnut Creek CA,
using ABI 3730 machines.
                                                                                  TTGATCCCATGAGTCCAATTTTCACCGAGCGTGAGCGAATCCAGGTCCTGTTATCAGATC
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                                          TIGATCCATIGAGCCCGATCTTCACCGAGCGTGAGCGAATCCAGGTTGCGTTATCAGATC
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Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
Asmundaon Hall, UCD, Davis, CA 95616, USA
Pax: 1-(530)-742-1742
Pax: 1-(530)-752-9659
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/clone="CLPX8050"
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/strain="PI-274378"
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DW093963

921 bp mRNA linear EST 22-DEC-2005 CLPY5158.bl L17.abl CLP (XYZ) lettuce perennis Lactuca perennis cDNA clone CLPY5158, mRNA sequence.

DW093963.1 GI:83891883
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DW094502 922 bp mRNA linear EST 22-DEC-2005
CLPY5600 bl G24.abl CLP(XYZ) lettuce perennis Lactuca perennis CDNA
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
atterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Lactuca.
I Cases I to 923)
I Cases, Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevaller, P., Ziegle, J.,
Blison, P., Kolkman, J., Slabudyh, M.S., Livingston, K., Zhou, Y.,
Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTS from the Compositae Genome Project
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University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
Library was sequenced at Joint Genome Institute, Walnut Creek CA, using ABI 3730 machines.
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/clone_lab="CLPKXXZ] lettuce perennis"
/noce="Vector: pBECDNASfiAB; The standard library was
constructed from multiple sources of RNA from a singl
                                                                             562 criciraacaacccaccresiceacrericacriresisrrassirascrissecrasserr
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Unpublished (2002)
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/strain="PI-274378"
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/note="Vector: pBRcDNASfiAB; The standard library was
constructed from multiple sources of RNA from a single
genotype. cDNAs were then size-fractionated, directionally
cloned into a custom medium-copy vector and
transformations made with three size classes
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                                              Eukaryota parameter, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; campanulids; Asterales; Asteraceae; Cichorioae; Lactuca.

1 (Dases i to 921)

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.
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                                                                                                                                                                                                                                                                                                                                                                         Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
1-1: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
Library was sequenced at Joint Genome Institute, Walnut Creek CA,
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                                                                                                                                                                                                                                                                                                                                                    Contact: Alexander Kozik [R.W.Michelmore]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="CLPYS158"
/lab host="E.coli"
/clone_lib="CLP(XYZ) lettuce
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Unpublished (2002)
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Location/Qualifiers
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/strain="PI-274378"
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/lab_host="E.coli"

Clone lib="CLP(XXZ) lettuce perennis"

/clone lib="CLP(XXZ) lettuce perennis"

/note="Vector: pBRcDNASflAB; The standard library was

constructed from multiple sources of RNA from a single

genotype. cDNAs were then size-fractionated, directionally

cloned into a custom medium-copy vector and

transformations made with three size classes
CLPY8633.b1 B23.ab1 CLP(XYZ) lettuce perennis Lactuca perennis cDNA clone CLPY8\overline{6}33, mRNA sequence. DW097606.
                                                                                                                                                           Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
asterids, campanulids, Asterales, Asteraceae, Cichorioideae;
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(Cases 1 to 927)

(Rozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J.,
Rlison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-742-1859
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
Library was sequenced at Joint Genome Institute, Walnut Creek
using ABI 3730 machines.
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/strain="PI-274378"
/db_xref="taxon:43195"
/clone="CLPY8633"
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    genotype. CDNAs were then size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with three size classes (X-large,Y-medium and Z-small) to minimize size bias due to differential transformation efficiency. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/"
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
Library was sequenced at Joint Genome Institute, Walnut Creek CA,
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1 (bases 1 to 922)

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J.,
Lin, H., van Damme, M., Jabaudh, M.S., Livingston, K., Zhou, Y.,
Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
AGTGACTACCAATGGATTGATGATACAGTCGGCTTCATCGTTCACTCCGCTCTCCTCACC
                                           CCTTACTTTCTTGGAAATACAGCCATCGAAAGCACCATGCAAACACAAATTCACTCGAA
                                                           CCTTATTTCTCTTGGAAATACAGCCATCGAAATCACCATGCCAACACAAAATTCACTTGAT
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Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
University of California at Davis (UCD)
Asmundason Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
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constructed from multiple sources of RNA from a single genotype. CDNAs were then size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with three size classes (X-large, Y-medium and Z-small) to minimize size bias due to differential transformation efficiency. Details of each source of RNA, and library construction can be
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/clone_lib="CLP(XYZ) lettuce perennis"
/note="Vector: pBRcDNASflAB; The standard library was
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                                                                                                                                                                                                                                                                                                                                  35.0%; Score 492.2; DB 10; Length
75.8%; Pred. No. 3.3e-114;
tive 0; Mismatches 194; Indels
                                                                                                                                                                                                                                                            obtained at http://cgpdb.ucdavis.edu/
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999

726 829 786 889

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928 bp mRNA linear EST 22-DEC-2005 CLPY13180.bl H07.abl CLP(XYZ) lettuce perennis Lactuca perennis DNOS clone CLPY13180, mRNA sequence.
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CAAGCTAGCATCCTCACTGGCTTATGGGTCATCGGTCATGAATGCGGTCACCATGCCTTT 372
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Department of Vegetable Crops, R.W.Michelmore Lab
Department of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Enail: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
Library was sequenced at Joint Genome Institute, Walnut Creek CA, using ABI 3730 machines.
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1 (base 1 to 928)

Kozik, Michelmore, R.W., Knapp, S., Marvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J.,
Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower EST$ from the Compositae Genome Project
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Unpublished (2002)
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/note="Vector: pBRcDNASfiAB; The standard library was
/note="Vector: pBRcDNASfiAB; The standard library was
constructed from multiple sources of RNA from a single
genotype. CDNAs were then size-fractionated, directionally
cloned into a custom medium-copy vector and
transformations made with three size classes
(X-large, Y-medium and Z-small) to minimize size bias due
to differential transformation efficiency. Details of
each source of RNA and library construction can be
obtained at http://cgpdb.ucdavis.edu/"
                                                906 bp mRNA linear EST 22-DEC-2005 CLPY4893.bl 124.abl CLP(XYZ) lettuce perennis Lactuca perennis cDNA CLDV4893, mRNA sequence.
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
Library was sequenced at Joint Genome Institute, Walnut
using ABI 3730 machines.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Pax: 1-(530)-742-1742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Alexander Kozik [R.W.Michelmore]
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clone="CLPY4893"
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/strain="PI-274378"
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DW090169 898 bp mRNA linear EST 22-DEC-2005 CLPY14207.bl N24.abl CLP (XYZ) lettuce perennis Lactuca perennis cDNA clone CLPY14207, mRNA sequence.
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fnote="Vector: pRRCDNASfiabs The standard library was
constructed from multiple sources of RNA from a single
genotype. cDNAs were then size-fractionated, directionally
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: akczikoatgc.org [michelmore@vegmail.ucdavis.edu]
Library was sequenced at Joint Genome Institute, Walnut Creek CA,
using ABI 3730 machines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rieseberg, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 808 GTGACCTGCATATATGGAGTACCAGTGCTAGGCGTATTTATCTTTTCGTTTTGATCACG
                                              TATCTGCACCACACATCTGTCGTCACCCCATTACGATTCAACCGAATGGAACTGGATC
                                                                 Cichorieae; Lactuca.

1 (bases 1 to 898)

Kozik, A., Michelmore, R.W., Knapp, S., Marvienko, M., Rieseberg, L.
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J.,
Ellison, P., Kolkman, J., Slabbaugh, M.S., Livingston, K., Zhou, Y.,
Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
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Pred. No. 2e-112;
0; Mismatches 179; Indels
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Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1- (530)-742-1742
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/clone="CLPY14207"
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/note="Vector: pBRcDNASfiAB; The standard library was
/note="Vector: pBRcDNASfiAB; The standard library was
constructed from wultiple sources of RNA from a single
genotype. CDNAS were then size-fractionated, directionally
cloned into a custom medium-copy vector and
transformations made with three size classes
(X-large, Y-medium and Z-small) to minimize size bias due
to differential transformation efficiency. Details of
each source of RNA and library construction can be
obtained at http://cgpdb.ucdavis.edu/"
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                             organism="Lactuca perennis"
                                              /mol_type="mRNA"
/strain="PI-274378"
/db_xref="taxon:43195"
/clone="CLPY13180"
                                                                                                                                        /lab_host="E.coli"
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/lab host="B.col" |
/lab host="B.col" |
/clone lib="CLP(XXZ) lettuce perennis" |
/clone lib="CLP(XXZ) lettuce of RNA from a single genotype. cDNAs were then size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with three size classes (X-large, Y-medium and Z-small) to minimize size bias due to differential transformation efficiency. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/"
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Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundaon Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Bmail: akozik@argo.org [michelmore@vegmail.ucdavis.edu]
Library was sequenced at Joint Genome Institute, Walnut
using ABI 3730 machines.
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                                                                                                                                                                                                                                    organism="Lactuca perennis"
                                                                                                                                                                                                                                                     /mol_type="mRNA"
/strain="PI-274378"
/db_xref="taxon:43195"
/clone="CLPY13349"
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Location/Qualifiers
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1 (bases 1 to 893)

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevaller, P., Ziegle, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L. and Bradford, K.
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Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterida; campanulida; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Lactuca.
1 (bases I to 919)
1 (bases I to 919)
1 (bases, Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J.,
Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
115 GATCCATCTAAGGACAACGATATACTAAAACGTGTCCCGGTTGA---GCCACCATTCTCA 171
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CLPY13299.bl E14.abl CLP(XYZ) lettuce perennis Lactuca perennis
CDNA clone CLPY13299, mRNA sequence.
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/db_xref="taxon:43195"
/clone="CLPY8961"
/lab_host="E.col1"
/clone lib="CLP(XZ) lettuce perennis"
/clone lib="CLP(XZZ) lettuce perennis"
/clone lib="CLP(XZZ) lettuce perennis"
/note="Vector: pBRcDNASfiAB; The standard library was
constructed from multiple sources of RNA from a single
genotype. cDNAs were then size-fractionated, directionally
cloned into a custom medium-copy vector and
transformations made with three size classes
(X:large,Y-medium and Z-small) to minimize size bias due
to differential transformation efficiency. Details of
each source of RNA and library construction can be
obtained at http://cgpdb.ucdavis.edu/"
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                                                                          Cichorieae; Lactuca.

(Cichorieae; Lactuca.

(Cichorieae; Lactuca.

(Cichorieae; Lo 942)

(Mozik, M., Micholmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.

Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J.,

Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,

Lai,Z., Church,S., Jackson,L. and Bradford,K.

Lettuce and Sunflower ESTs from the Compositae Genome Project

http://compgenomics.ucdavis.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
Library was sequenced at Joint Genome Institute, Walnutusing ABI 3730 machines.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Vegetable Crops, R.W.Michelmore University of California at Davis (UCD) Asmundaon Hall, UCD, Davis, CA 95616, USA Per: 1-(530)-742-1742 Pax: 1-(530)-752-9659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Alexander Kozik [R.W.Michelmore]
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/strain="PI-274378"
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EST 22-DEC-2005

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/notes_tropy backgraphs, the standard library was constructed from multiple sources of RNA from a single sources of RNA from a single spencype. CDNAs were then size fractionated, directionally cloned into a custom medium-copy vector and transformations made with three size classes (X-large, Y-medium and Z-small) to minimize size bias due to differential transformation efficiency. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/"
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Lactuca perennis
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
asterids, campanulds, Asterales, Asteraceae, Cichorioideae,
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1 (bases 1 to 908)

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevaller, P., Ziegle, J.,
Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K.,
Ellison, P., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunfilower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
                                                                                                                                                                                                                                    741 GGICTICTIGCCGICTITITATGCAATTAAACTIGCTGTAGAAAGAAAGAAAGGAGTIGCTIGG
                                                                                                                                                                                                                                                                                       GTGATGTGCATGTATGGAGTTCCAGTGATAGGTCTGAATTCCTTCATTATCGTAATCACT
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GATCCATTGAGCCCGATCTTCACCGAGCGTGAGCGAATCCAGGTTGCGTTATCAGATCTT
                                                                                                                                          GATCCGATGAGCCCAATTTTCACCCAACGTGAACGGATTCAAGTTCTGCTATCGGATTTT
                                                                                                                                                                                          Contract: Alexander Kozik [R.W.Michelmore]
Contract: Alexander Kozik [R.W.Michelmore Lab
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
Library was sequenced at Joint Genome Institute, Walnut Creek using ABI 3730 machines.

Location/Qualifiers
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/strain="PI-274378"
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/note="Vector: pBRcDNASfiAB; The standard library was constructed from multiple sources of RNA from a single genotype. CDNAS were then size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with three size classes
(X-large, Y-medium and Z-small) to minimize size bias due to differential transformation efficiency. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/"
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                                                                                Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
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Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1142
Fax: 1-(530)-742-1659
Email: akozik@atgc.org [michelmore@vegmail:ucdavis.edu]
Library was sequenced at Joint Genome Institute, Walnut Creek (using ABI 3330 machines.
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                         the Compositae Genome Project
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75.8%; Pred. No. 2.1e-111;
tive 0; Mismatches 193; Indels
Lai,Z., Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower BSTs from the Composita
http://compgenomics.ucdavis.edu/
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="E.coli"
/clone_lib="CLP(XYZ) lettuce
                                                                                                                                                                                                                                                                                                                                                                  organism="Lactuca perennis"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:43195"
/clone="CLPY13299"
                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/strain="PI-274378"
                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        637; Conservative
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Matches 63
                                                                        JOURNAL
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1. Similarity 75.6%; Pred. No. 2.7e-111; 625; Conservative 0; Mismatches 193; Indels 9; Gaps 2;	10 GATCGAATGAAAGATCATGATGACGAGAGCCCCGATTGATCCGGCGCCATTCTCG 169	91 GATCCATCTAAGGACAACGATATACTAAAACGTGTCCCGGTTGAGCCACCATTCTCA 147	10 TTAAGTGATCTAAAGAAAGCAATCCCTGCACATTGCTTCCGGGGATCCGCCGTCTGGTCA 229	TCCTGCTACGTAGTTCAGGATCTCATTATCACCTTCCTTTTATACACGGTCGCCAACACC			68 TATATTCCTATTCTTCCTTTTCCTCTAGCTTAGCTAGGCCAGTTTACTGGTTCTGC 327	CAATCITGCAICCTCACTGGTTTATGGGTCCTCGGCCATGAATGCGGCCATCATGCCTTT	28 CAAGCTAGCATTCTTACTGGCTTATGGGTCATGGGTCATGAATGTGGTCACCATGCTTT 387	AGTGAGTACCAGTGGATTGATAACGCCGTTGGATTCGTCCTCCATTCGGCTCTCCTCACC	88 AGTGACTACCAATGGATTGATGATACAGTCGGCTTCATCGTTCACTCCGCTCTCCTCACC 447		48 CCTIATTTCTCTTGGAAATACAGCCATCGAAATCACCATGCCAACACAAATTCACTTGAT 507		08 AACGATGAAGTITACATTCCTAAACGCAAGTCCTAAGTCACGCTTTACTCAAAA 561	90 ITTCTIGACAACACGCCTGGTCGAATCCTCATCTTGGTCATGTTAACCTTAGGATTT 649	62 CTTCTTAACAACCCACCTGGTCGAGTGTTCACTTTGGTGTTTAGGTTGACCCTAGGGTTT 621	50 CCTTTATACCACCTAGAATGTTTCAGGCAAGAAGTACGATAGATTTACCAACCA	22 CCTTTATACCTCTTAACTAATATTTCTGGCAAAAATACGGAAGGTTTGCCAACCACTTT 681	10 GAICCAITGAGCCCGAICTICACCGAGCGTGAGCGAATCCAGGTTGCGTTATCAGAICTT 769	82 GATCCGATGAGCCCAATTTTCACCCAACGTGAACGGATTCAAGTTCTGCTATCGGATTTT 741	70 GGTAICGTIGCAGIGITITIACGGACTCAAGTITCTIGTACAAACAAAAGGAITIGGITIGG	42 GGTCTTCTTGCCGTCTTTTATGCAATTAAACTTGCTGTAGAANGAAAGGAGTTGCTTGG 801	30 GTGATGTGCATGTATGGAGTTCCAGTGATAGGTCTGAATTCCTTATCGTAATCACT 889	02 GIGACCIGCATATAIGGAGIACCAGIGCIAGGCGIAITIAICITITICGIITIGAICAGG 861	190 TATCTGCACCACACACATCTGTCACCCCATTACGATTCAACCGA 936	isz ratriscaccacacreateatrscercacratsaricaaces 908
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Search completed: September 25, 2006, 01:03:36 Job time : 7207 secs



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September 25, 2006, 00:03:35 ; Search time 300 Seconds (without alignments) 8285.225 Million cell updates/sec
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/ EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/ EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/ EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/ EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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/ EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
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                                                                                                                                                                                                                                                                                                                                                                                           version 5.1.9
- 2006 Biocceleration Ltd.
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Maximum DB seq length: 2000000000
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Result No.	Score	Query Match	Query Match Length	DB	ΙD	Description
-	467	33.2	6220	7	US-11-369-993-3	Sequence 3, Appli
7	464.2	33.0	1647	œ	US-11-216-545-4819	Sequence 4819, Ap
Э	462.6	32.9	1517	6	US-11-056-355B-52711	52711,
4	462.6	32.9	1669	ω	US-11-216-545-4818	Sequence 4818, Ap
Ŋ	426.2	30.3	1451	6	US-11-056-355B-39927	Sequence 39927, A
9	426.2	30.3	1459	σ	US-11-056-355B-98545	
7	426.2	30.3	1459	σ	US-11-056-355B-109784	Sequence 109784,
80	426.2	30.3	1617	9	US-10-547-086-17	Sequence 17, Appl
σ	425.2	30.2	1389	σ	US-11-056-355B-75573	Sequence 75573, A
10	424.6	30.2	1451	σ	US-11-056-355B-42535	Sequence 42535, A
11	423	30.1	1411	σ	US-11-056-355B-28874	Sequence 28874, A
12	423	30.1	1411	σ	US-11-056-355B-32464	Sequence 32464, A
13	412.6	29.3	1391	σ	US-11-056-355B-36365	Sequence 36365, A
14	402.2	28.6	1155	æ	US-11-340-318-1	Sequence 1, Appli
15	400	28.4	1155	œ	US-11-340-318-5	Sequence 5, Appli
16	398.4	28.3	1155	œ	US-11-340-318-3	m
17	390.2	27.8	1470	80	US-11-216-545-2763	Sequence 2763, Ap
18	390.2	27.8	4497	7	US-11-369-993-15	Sequence 15, Appl
19	390.2	27.8	4497	7	US-11-376-328-4	Sequence 4, Appli
20	384.8	27.4	1855	80	US-11-058-746-3	Sequence 3, Appli
21	379	27.0	1561	œ	US-11-216-545-2762	Seguence 2762, Ap
22	372	26.5	1583	7	US-11-364-183-6	Sequence 6, Appli
23	364	25.9	921	σ	US-11-133-075-79	Sequence 79, Appl

Sequence 72, Appl	Seguence 22074, A	Seguence 14683, A	Sequence 20235, A	Sequence 38512, A .	Sequence 1515, Ap	Sequence 5992, Ap	Sequence 15292, A	Sequence 28919, A	Seguence 8023, Ap	Sequence 4582, Ap	Seguence 5634, Ap	Sequence 8768, Ap	Sequence 12636, A	Sequence 8217, Ap	Seguence 4008, Ap	Seguence 2, Appli	Sequence 7274, Ap	Seguence 1, Appli	Sequence 7328, Ap	Sequence 7993, Ap	Sequence 582, App
US-11-133-075-72	US-10-449-902-22074	US-10-449-902-14683	US-10-449-902-20235	US-10-953-349-38512	US-11-056-355B-1515	US-11-056-355B-5992	US-11-056-355B-15292	US-10-953-349-28919	US-10-449-902-8023	US-11-056-355B-4582	US-11-056-355B-5634	US-11-292-078-8768	US-11-292-078-12636	US-11-292-078-8217	US-10-449-902-4008	US-11-058-746-2	US-11-292-078-7274	US-11-058-746-1	US-11-292-078-7328	US-11-292-078-7993	US-11-314-834-582
6 068	9 001	9 9581	1361 6	1764 6	1764 9	1764 9	1764 9	1441 6	1267 6	6 9991	6 9941	620 7	592 7	590 7	1177 6	544 8	601 7	543 8	637 7	584 7	363 7
5 25.4	24.6	24.6	24.0	24.0	24.0	24.0	. 24.0	23.9	23.8	23.3	23.1	16.4	15.5		2 14.6 1				2 12.1	4 11.3	4 10.7
357.6	345.8	345.8	337.8	337.2	337.2	337.2	337.2	335.4	335.2	327.8	324.6	230.2	218	211	205.2	180.8	178.4	17	170.2	158.4	150.4
24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	c 43	c 44	45

## ALIGNMENTS

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Sequence 3, Application US/11369993

Sequence 3, Application US/11369993

Publication No. US20060191042A1

GENERAL INFORMATION:

APPLICANT: Fillatti, Johnne, J.

ITLE OF INVENTION: With Modified Polyunsaturated Fatty Acids

ITLE OF INVENTION: With Modified Polyunsaturated Fatty Acids

ITLE OF INVENTION: With Modified Polyunsaturated Fatty Acids

FILE REFERENCE: 16518.056

CURRENT APPLICATION NUMBER: US/11/369,993

CURRENT FILING DATE: 2006-03-08

FRIOR APPLICATION NUMBER: US 60/151,224

FRIOR APPLICATION NUMBER: US 60/151,224

FRIOR PILING DATE: 1999-08-26

FRIOR PILING DATE: 1999-12-17

FRIOR PILING DATE: 1090-08-11

FRIOR PILING DATE: 2000-08-11

FRIOR FILING DATE: 2000-08-11
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Pred. No. 2e-90;
0; Mismatches 445; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 62.4%;
Matches 750; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Glycine max US-11-369-993-3
US-11-369-993-3
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Publication No. US20060135758A1
GENERAL INFORMATION:
APPLICANT: MONSANTO Technology, LLC
APPLICANT: MONSANTO Technology, LLC
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Wu, Kunaheng
TITLE OF INVENTION: Single Nucleotide Polymorphic Markers and Methods of Genotyping
TITLE OF INVENTION: Soybeans.
FILE REFERENCE: 38-21 (53659)B
CURRENT APPLICATION NUMBER: US/11/216,545
CURRENT APPLICATION NUMBER: US 60/606,062
PRIOR FILING DATE: 2005-08-31
PRIOR FILING DATE: 2004-08-31
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 4819
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Publication No. US20060150283A1
GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
APPLICANT: Brover, Vyacheslav
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR PILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NOS: 119966
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| LOCATION: (1)..(1517)

| OTHER INFORMATION: Ceres Seq. ID

| US-11-056-3558-52711
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US-11-056-355B-52711
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564 AGCTCAGGACTTACTCCACATACGAATTTCTTGACAACACGCCTGGTCGAATCCTCATCT 623
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APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Defermined DNA Fragments and Corresponding
TITLE OF INVENTION: Sequence Defermined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REPERENCE: 2750-1590PUS2
CURRENT PELLING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR PILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 39927
LENGTH: 1451
                                                                                                                                          TGGTCATCATGTTAACCTTAGGATTTCCTTTATACCTCTTAACGAATGTTTCAGGCAAGA
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NAME/KEY: misc_feature
LOCATION: (1)...(1451)
FEATURE INFORMATION: Ceres Seq. ID no. 12370299
FEATURE:
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                                                                                                                                                                                                                                      Sequence 4818, Application US/11216545
Publication No. US20060135758A1
GENERAL INFORMATION:
APPLICANT: MOLEAIGN, Paul L
APPLICANT: MCLEAIGN, Paul L
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: W. Kunsheng
ITLE OF INVENTION: Single Nucleotide Polymorphic Markers and Methods of Genctyping
TITLE OF INVENTION: Soybeans.
FILE REPERENCE: 38-21 (53659)8
CURRENT FILING DATE: 2005-08-31
PRIOR APPLICATION NUMBER: US 60/606,062
PRIOR PILING DATE: 2004-08-31
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62.2%; Pred. No. 1.3e-89;
tive 0; Mismatches 449;
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SOFTWARE: Patentin version 3.2
SEQ ID NO 4818
LENGTH: 1669
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Matches 748; Conservative
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                                                                              1234 AGT 1236
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US-11-216-545-4818
          TGT
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                                                                                                                                                                                       TATAGGGAGGCAAAGGAGTGTATCTATGTAGAACCGGACAGGGAAGGTGACAAGAAAGGT 1277
                                                                                                                                                                                                                                                                                                                                       Sequence 98545, Application US/11056355B
; Sequence 98545, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590FUS/
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 98545
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in SEQ ID NO 52711
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61.0%; Pred. No. 7.5e-82;
live 0; Mismatches 448;
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OTHER INFORMATION: Ortholog
OTHER INFORMATION: as cited
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NAME/KEY: misc_feature
LOCATION: (1)..[1459)
OTHER INFORMATION: Ceres SE
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NAME/KEY: misc_feature
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Best Local Similarity 61.0
Matches 711; Conservative
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                                                                                                   Score 426.2; DB 9; Length
Pred. No. 7.5e-82;
0; Mismatches 448; Indels
                                 of Ceres SEQ ID NO 15177298 in SEQ ID NO 52711
                                                                                                   Query Match 30.3%;
Best Local Similarity 61.0%;
Matches 711; Conservative
   NAME/KEY: misc_feature
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                                                                                                                                                                                                                                         FEATURE:
| NAME/KEY: misc_feature
| CCATION: (1)...(1459)
| OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 15177298
| OTHER INFORMATION: as cited in SEQ ID NO 52711
| US-11-056-3558-109784
                                                                                                                                                                                                                     Seq. ID no. 13600976
                                                                                                  TYPE: DNA ORGANISM: Arabidopsis thaliana
  PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 109784
LENGTH: 1459
                                                                                                                                                 FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1459)
OTHER INFORMATION: Ceres
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US-11-056-355B-109784

i Sequence 109784, Application US/11056355B

j Sequence 109784, Application US/11056355B

j Publication No. US20060150283AI

j GENERAL INFORMATION:
 APPLICANT: Brover, Vyacheslav

j APPLICANT: Alexandrov, Nickolai

TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding

TITLE OF INVENTION: Polypeptides Encoded Thereby

TITLE OF INVENTION: Polypeptides Encoded Thereby

TITLE OF UNDENTION: US111/056,355B

CURRENT APPLICATION NUMBER: US111/056,355B

CURRENT FILING DATE: 2005-02-14

PRIOR APPLICATION NUMBER: 60/544,190
ACTGGTATCTGGGTCATAGCCCACGAATGCGGTCACCACGCATTCAGCGACTACCAATGG
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Fublication No. US20060150283A1
GENERAL INFORMATION:
APPLICANT: Brown, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding;
TITLE OF INVENTION: Polypeptides Encoded Thereby
CCTCAGCCTCTCTTACTTGGCTTGGCCACTCTATTGGGCCTGTCAAGGCTGTGTCTCTA
                                                                                                                                                                                                                                                   AAGTATAGTCATCGCCGTCACCATTCCAACACTGGATCCCTCGAAAGAGAGATGAAGTATTT
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    GGAGTTCCAGTGATAGGTCTGAATTCCTTCATTATCGTAATCACTTATCTGCACCACACA
                                                                               CATCTGTCGTCACCCCATTACGATTCAACCGAATGGAACTGGATCAAAGGAGCCTTGACC
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Pred. No. 7.7e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17, Application US/10547086
Publication No. US20060195919A1
GENERAL INFORMATION:
ITILE OF INVENTION: Arabidopsis promoters
FILE REFERENCE: CD-075-PCT
CURRENT APPLICATION NUMBER: US/10/547,086
CURRENT PILING DATE: 2005-08-26
PRIOR APPLICATION NUMBER: EP 03075587.0
PRIOR FILING DATE: 2003-02-7
NUMBER OF SEC ID NOS: 36
SOFTWARE: PatentIn version 3.1
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NAME/KDY: misc_feature
THER INFORMATION: TC160765 (PRO0193)
US-10-547-086-17
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ORGANISM: Arabidopsis thaliana
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Best Local Similarity
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                                                                            903
                                                                                                                                                                                                 Sequence 42535, Application US/11056355B

Sublication No. US20060150283A1

GENERAL INFORMATION.

APPLICANT: Brover, Vyacheslav

APPLICANT: Alexandrov, Nickolai

TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding

TITLE OF INVENTION: Polypeptides Encoded Thereby

TITLE OF INVENTION: POLYpeptides Encoded Thereby

TITLE OF INVENTION: US/11/056,355B

CURRENT PAPLICATION NUMBER: 2005-02-14

PRIOR APPLICATION NUMBER: 60/544,190

PRIOR APPLICATION NUMBER: 60/544,190

PRIOR APPLICATION NUMBER: 2004-02-13

NUMBER OF SEQ ID NOS: 119966

SEQ ID NO 42535
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    TITACGGACTCAAGITICTIGIACAAACAAAAGGAITIGGITGGGTGAIGTGCATGTAIG
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LOCATION: (1)...(1451)
COTHER INFORMATION: Ceres Seq. ID no. 12337750
FEATURE: Misc_feature
NAME/KEY: misc_feature
COCATION: (1)...(1451)
COTHER INFORMATION: Ortholog of Ceres SEQ ID NO 15177298
COTHER INFORMATION: as cited in SEQ ID NO 52711
US-11-056-3558-42535
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ORGANISM: Arabidopsis thaliana
FEATURE:
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US-11-056-355B-42535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 TCAGAAATCTGGGAGAAGGTAGCAGAATGTCGGATTCATATGATGATCGAATGAAGATC 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    310 grgacarcarraragecrecargerreractrocáreceaecaarractrerereree 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CICCICCICIAGITIACITAGCAIGGCCGGITIACIGGITITGCCAAICITGCAICCICA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 CTGGTTTATGGGTCCTCGGCCATGATGCGGCCATCATGCCTTTAGTGAGTACCAGTGGA 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATACAGCCATCGAAAGCACCATGCAAACACAAATTCACTCGAAAACGAGGAAGTTTACA 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               250 AAGCAATCCCGCCATTGTTTCAAACGCTCAATCCCTCGCTCTTTCTCCTACCTTATCA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         370 crcaeccrcrcrracrregerregecacrcrarregecrerereaegererera 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 ccaacacaaaagcargraccaracagaaaccacrrrcrcagragaaarcraaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 ATGATATGGACGAACGAGCCCCGATTGATCCGGCGCCATTCTCGTTAAGTGATCTAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 AGGATCTCATTATCACCTTCCTTTTATACACGGTCGCCAACACCTACATTCCTCACCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGATAACGCCGTTGGATTCGTCCTCCATTCGGCTCTCCTCACCCCTTACTTTTCTTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  610 rcccaaagcagaaarcagcaarcaagragracgaaaarac----crcaacaacccc
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30.2%; Score 425.2; DB 9; Length 1389;
Best Local Similarity 61.0%; Pred. No. 1.2e-81;
Matches 710; Conservative 0; Mismatches 448; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc_feature
CCATION: (1)..(1389)
OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 15177298
OTHER INFORMATION: as cited in SEQ ID NO 52711
US-11-056-355B-75573
                                                                                                                                                                                                                                                                                                                                                                                                                               NAMEKEY: misc feature
LOCATION: (1). (1389)
OTHER INFORMATION: Ceres Seq. ID no. 6444000
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 75573
LENGTH: 1389
                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Arabidopsis thallans
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                                                                                                                     GENERAL INFORMATION:

APPLICANT: Brover, Vyacheelav

APPLICANT: Alexandrov, Nickolai

TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding

TITLE OF INVENTION: Polypeptides Encoded Thereby

TITLE OF INVENTION: Polypeptides Encoded Thereby

TITLE OF INVENTION: 1950PUS2

CURRENT APPLICATION NUMBER: 105/11/056,355B

CURRENT APPLICATION NUMBER: 60/544,190

PRIOR APPLICATION NUMBER: 60/544,190

PRIOR PILLING DATE: 2004-02-13

NUMBER OF SEQ ID NOS: 119966

SEQ ID NO 28874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         605 CCTGGTCGAATCCTCATCTTGGTCATCATGTTAACCTTAGGATTTCCTTTATACCTCTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rccagaaacargegrecaggregaagaargccegrrccracrrcrrccaagaaarcegaa
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Best Local Similarity 60.9%; Pred. No. 3.6e-81;
Matches 709; Conservative 0; Mismatches 450; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
| NAME/KEY: misc_feature
| LOCATION: (1). (1411)
| OTHER INFORMATION: Ceres Seq. ID no. 12321215
| FEATURE:
| FEATURE:
| NAME/KEY: misc_feature
| LOCATION: (1). (1411)
| OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 15177298
| OTHER INFORMATION: as cited in SEQ ID NO 52711
| US-11-056-355B-28874
                                                          Sequence 28874, Application US/11056355B
Publication No. US20060150283A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Arabidopsis thaliana
                         US-11-056-355B-28874
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                 Score 423; DB 9; Length 14
Pred. No. 3.6e-81;
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APPLICANT: Brover, Vyacheslav
APPLICANT: Brover, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REPERBNCE: 2750-1590F082
CURRENT FILING DATE: 2005-02-14
PRIOR FILING DATE: 2004-02-13
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 32464
LENGTH: 1411
                                                                     FEATURE:
NAME/KEY: misc_feature
CCATION: (1)..(1411)
COTHER INFORMATION: Ortholog of Ceres SEQ ID NO 15177298
OTHER INFORMATION: as cited in SEQ ID NO 52711
(US-11-056-3558-32464
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US-11-056-355B-32464
// Sequence 32464, Application US/11056355B
// Publication No. US20060150283A1
// GENERAL INFORMATION:
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Publication No. US20060137040A1
CENERAL INFORMATION:
APPLICANT: DeBonte, L. et al.
TITLE OF INVENTION: CANOLA OIL HAVING INCREASED OLEIC ACID AND TITLE OF INVENTION: DECREASED LINOLENIC ACID CONTENT NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C., P.A.
STREET: 60 South Sixth Street, Suite 3300
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGGTATCTGGGTCATAGCCCACGAATGCGGTCACCACGCATTCAGCGACTACCAATGGC 489
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                                          1166 ATAAAGCCAATTCTGGGAGACTATTACCAGTTCGATGGAACACCGTGGTAGTGGGCGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Brover, Vyacheslav
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
TILLE OF INVENTION: 2009-052
CURRENT FILLE SPERCE: 2750-1590P022
CURRENT APPLICATION NUMBER: US/11/056,355B
PRIOR FILLING DATE: 2005-02-14
PRIOR FILLING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
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CHER INFORMATION: Ortholog of Ceres SEQ ID NO 15177298

CTHER INFORMATION: as cited in SEQ ID NO 52711

US-11-056-355B-36365
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60.9%; Pred. No. 6e-79;
iive 0; Mismatches 449;
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OTHER INFORMATION: Ceres Seq.
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Matches 709; Conservative
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NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
US-11-056-355B-36365
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STATE: MINNEADLES

COUNTRY: Winneapolis

COUNTRY: WAS APPOLED

SEQUENCE: APPLICANT: DEBORTE. L. et al.

TITLE OF INVENTION: DECREASED LINOLENIC ACID CONTENT

NUMBER OF SEQUENCES:

COTTY: Minneapolis

STATE: MN

COUNTRY: USA
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/340,318
FILING DATE: 26-JAN-2006
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/907,608
FILING DATE: 08-AUG-1997
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COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
SUBMENT APPLICATION DATA:
APPLICATION NUMBER: US/11/340,318
FILING DATE: 26.54N-2006
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/907,608
FILING DATE: 08.40G-1997
PRIOR APPLICATION NUMBER: 08/675,650
FILING DATE: 03.40L-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lundquist, Romald C.
REGISTRATION NUMBER: 07148/042002
TELEPHONE: 612/385-5070
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                    APPLICATION NUMBER: 08/675,650
FILING DATE: 03-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: LAINGGAISER: 37,875
REGISTRATION NUMBER: 37,875
REFERENCE/DOCKET NUMBER: 07148/042002
TELECOMMUNICATION INFORMATION:
TELEPAX: 612/289-9696
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 1155 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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ORIGINAL SOURCE:
ORGANISM: Brassica napus
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Best Local Similarity 60.4
Matches 699; Conservative
PRIOR APPLICATION DATA:
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MOLECULE TYPE: DNA
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Sequence 27, Appl
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Sequence 33, Appl
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Sequence 10, Appl
Sequence 1, Appli
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Sequence 19, Appl
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Sequence 6, Appli
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Sequence 9, Appli
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Sequence 12, Appl
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(c) 1993 - 2006 Biocceleration Ltd.
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Listing first 45 summaries
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Sequence 11, Appli
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Sequence 1, Application US/10622774

Publication No. US20050022270A1

GENERAL INFORMATION:

APPLICANT: University of Kentucky Research Foundation
APPLICANT: Hildebrand, David
APPLICANT: Hildebrand, David
TITLE OF INVENTION: RECOMBINANT STOKESIA EPOSYGENASE GENE
FILE REFERENCE: 050229-0377

CURRENT APPLICATION NUMBER: US/10/622,774

CURRENT FILING DATE: 2003-07-21

PRIOR APPLICATION NUMBER: 60/396,406

PRIOR APPLICATION NUMBER: 60/396,406

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn version 3.2
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Best Local Similarity 100.
Matches 1406; Conservative
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Publication No. US2005002227041

JEBURRAL INFORMATION:
APPLICANT: University of Kentucky Research Foundation
APPLICANT: Hildebrand, David
JAPPLICANT: Hatanka, Tomoko
TITLE OF INVENTION: RECOMBINANT STOKESIA EPOSYGENASE GENE
FILE REPERENCE: 050229-0377
CURRENT APPLICATION NUMBER: US/10/622,774
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: 60/396,406
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.2
SEQ ID NOS: 10
SEQ ID NOS: 10
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llarity 86.1%; Pred. No. 7.5e-228;
Conservative 0; Mismatches 155;
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                                                                                   TYPE: DNA ORGANISM: Veronia galamensis
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963; Conserv
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                                                                                             GCCCCATCTTCAGTGAGCGTGAACGAATCCAGGTCGTGCTATCGGATGTGGGTCTCATTG
                                                                                                                                                   GCCCGATCTTCACCGAGCGTGAGCGAATCCAGGTTGCGTTATCAGATCTTGGTATCGTTG
                                                                                                                                                                                                                                       | TGTATGGAGTTCCAGTGATAGGTCTGAATTCCTTCATTATCGTAATCACTTATCTGCACC
                         TCTTGACCAATATTTCAGGCAAGAATACCAAAGGTTTGCCAACCACTTTGATCCGTTGA
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APPLICANT: Ricek, Andrew P.
APPLICANT: Aloek, Andrew P.
APPLICANT: Davia-Aponte, Jennifer A.
APPLICANT: Britania, Merry B.
APPLICANT: McLaird, Merry B.
APPLICANT: Schtella, Rodolfo.
APPLICANT: Schtella, Rodolfo.
APPLICANT: Williams, Deryck J.
TITLE OF INVENTION: PLANTS MADE THEREFROM
FILE OF INVENTION: PLANTS MADE THEREFROM
FILE REPERRNCE: 12557-023001
CURRENT APPLICATION NUMBER: US/10/912,534
CURRENT FILING DATE: 2004-08-04
PRIOR PILING DATE: 2004-02-04
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 131
LENGTH: 1137
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Publication No. US20050172358A1
PRERAL INFORMATION:
APPLICANT: Verbsky, Michelle L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Stokesia laevis
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US-10-912-534-131
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US-10-912-534-131
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TATCAGATCTTGGTATCGTTGCAGTGTTTTACGGACTCAAGTTTCTTGTACAAAAG 818
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                                                                                                CCAACCACTITIGATCCATTIGAGCCCGATCTTCACCGAGCGTGAGCGAATCCAGGTTGCGT
                                                                                                                                    Sequence 27, Application US/10912534

Sequence 27, Application US/10912534

Publication No. US20050172358A1

GENERAL INFORMATION:
APPLICANT: Verbasky, Michelle L.
APPLICANT: Baublite, Catherine
APPLICANT: Baublite, Catherine
APPLICANT: Broila-Aponte, Jennifer A.
APPLICANT: Broila-Aponte, Jennifer A.
APPLICANT: McDia-Aponte, Jennifer A.
APPLICANT: McDia-M. McDelle Coutu
APPLICANT: McDia-M. McDelle Coutu
APPLICANT: McDia-M. Percy B.
APPLICANT: McDia-M. Percy B.
APPLICANT: Miliams, Deryck J.
TITLE OF INVENTION: PLANTS MADE THEREFROM
FILE REFERENCE: 12557-02301

CURRENT APPLICATION NUMBER: US/10/912,534

CURRENT FILING DATE: 2004-08-04

PRIOR FILING DATE: 2004-02-04

NUMBER OF SEQ ID NOS: 140

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 27

LENGTH: 1134
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Best Local Similarity
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; LOCATION: (1)
US-10-912-534-27
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US-10-912-534-27
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                                          1172 ATCGAGCAAGATGCAGCAGCAGCACAAGGGACATATTGGTACCATAAAATGTAA 1228
                                                                             1081 ATTGAACAAGATGCTGACTCTAAGCGAAACTTATTGGTATCATAAGATGTAA 1137
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APPLICANT: Baublite, Catherine
APPLICANT: Baublite, Catherine
APPLICANT: William Deryck J.
APPLICANT: William Deryck J.
APPLICANT: Milliam Deryck J.
APPLICANT: Milliam Deryck J.
APPLICANT: Hresko, Michelle Coutu
APPLICANT: McLard, Marry B.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC
TITLE OF INVENTION: AGENTS AND PLANTS NADE THEREFROM
FILE REFERENCE: 12557-016001
CURRENT PILLING DATE: 2004-02-04
PRIOR APPLICATION NUMBER: US 60/445,293
PRIOR PILLING DATE: 2003-02-05
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FeatSEQ for Windows Version 4.0
SEQ ID NO 27
LENGTH: 1134
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48.5%; Score 681.6; DB 8;
Best Local Similarity 78.0%; Pred. No. 4.3e-176;
Matches 835; Conservative 0; Mismatches 229;
                                                                                                                                                                                                                                                            // Sequence 27, Application US/10772227
// Publication No. US20040168213A1
// GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Stokesia laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: CDS
; LOCATION: (1)...(1131)
US-10-772-227-27
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APPLICANT: Baublite, Catherine
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                                                                         Sequence 33, Application US/10772227
Publication No. US20040168213A1
GENERAL INFORMATION:
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ORGANISM: Stokesia laevis
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879 TCGTAATCACTTATCTGCACCACACATCTGTCGTCACCCCATTACGATTCAACCGAAT
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1085 CAGATGAAGATACTGAACACAAGGGTGTTTACTGGTACCATAAAATGTAA 1134
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47.3%; Score 665.6; DB 10; Length
Best Local Similarity 77.1%; Pred. No. 1.1e-171;
Matches 825; Conservative 0; Mismatches 239; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Baublite, Catherine
APPLICANT: Rick, Andrew P.
APPLICANT: Rick, Andrew P.
APPLICANT: Applice, Jennifer A.
APPLICANT: Hresko, Michelle Coutu
APPLICANT: APPLICANT: Centella, Redelle Coutu
APPLICANT: APPLICANT: Sentella, Redery B.
APPLICANT: Williams, Deryck J.
TITLE OF INVENTION: PLANTS MADE THEREFROM
FILE REFERENCE: 12557-023001
CURRENT APPLICATION NUMBER: US/10/912,534
CURRENT APPLICATION NUMBER: US 10/772,227
PRIOR PILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 140
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
LENGTH: 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 33, Application US/10912534, Publication No. US20050172358A1, GENERAL INFORMATION:
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; LOCATION: (1).
US-10-912-534-33
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828 GGGTGATGTGCATGTATGGAGTTCCAGTGATAGGTCTGAATTCCTTCATTATCGTAATCA
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Sequence 6, Application US/10912534

Publication No. US200S0172358A1

SEMENTAL INFORMATION:
APPLICANT: Watherine
APPLICANT: Mandrew P.
APPLICANT: Machaird, Macrey B.
APPLICANT: Machaird, Macrey B.
APPLICANT: Watherine, Jennifer A.
APPLICANT: Machaird, Macry B.
APPLICANT: Watherine, Deryck J.
TITLE OF INVENTION: WOCLEIC ACIDS ENCODING ANTHELMINTIC AGENTS AND TITLE OF INVENTION: WOUCEIC ACIDS ENCODING ANTHELMINTIC AGENTS AND TITLE OF INVENTION: WHORER: US/10/912,534

CURRENT APPLICATION WUMBER: US/10/912,534

CURRENT FILING DATE: 2004-08-04

PRIOR FILING DATE: 2004-02-04

NUMBER OF SEC ID NOS: 140

SEC ID NOS: 140

SER DID NO 6
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46.8%; Score 657.8; DB 10;
Best Local Similarity 75.6%; Pred. No. 1.5e-169;
Matches 847; Conservative 0; Mismatches 262;
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US-10-912-534-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317 TTAGCGAGTACCAATGGGTTGACGACACTGTGGGCTTCATGGTCCACTCATTTCTCTCTA 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                377 CCCCGTATTTCTCGCGGAAATACAGTCACCGGAATCACCATGCCAACACAAGTTCCATCG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      528 AAAACGAGGAAGTTTACATTCCTAGAACTCAGTCCCAGCTCAGGACTTACTCCACATACG 587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 ATGATCGAATGAAAGATCATGATATGGACGAACGAGCCCCCGATTGATCCGGCGCCATTCT
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                                                                      APPLICANT: Verballor,
APPLICANT: Baublite, Catherine
APPLICANT: William, Deryck J.
APPLICANT: Milliam, Deryck J.
APPLICANT: Milliam, Deryck J.
APPLICANT: Milliam, Deryck J.
APPLICANT: Milliam, Deryck J.
APPLICANT: Hresko, Michelle Coutu
APPLICANT: Hresko, Michelle Coutu
APPLICANT: Michelle Coutu
APPLICANT: Michelle Coutu
APPLICANT: Michelle Coutu
APPLICANT: MILLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC
TITLE OF INVENTION: AGENTS AND PLANTS MADE THEREFROM
FILE REFERENCE: 12557-016001
CURRENT APPLICATION NUMBER: US 60/445,293
FRIOR FILING DATE: 2003-02-05
NUMBER OF SEQ ID NOS: 130
SOFTHARE: PSECSED FOR WINDOWS Version 4.0
SEQ ID NO 6
LENGTH: 1125
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Sequence 6, Application US/10772227
Publication No. US20040168213A1
GENERAL INFORMATION:
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Matches 847; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Crepis biennis
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LOCATION: (1)...(1122)
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APPLICANT: Singh, Surinder
APPLICANT: Lamman, Marit
APPLICANT: Stymne, Sten
TITLE OF INVENTION: FATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES THEREFOR IN MOD)
TITLE OF INVENTION: FATTY ACID METABOLISM
FILE REFERENCE: 26-98A
CURRENT APPLICATION NUMBER: US/09/981,124
CURRENT FILING DATE: 1098-04-14
PRIOR PILING DATE: 1098-04-14
PRIOR PLING DATE: 1099-04-15
PRIOR PELING DATE: 1997-04-15
PRIOR PELING DATE: 1997-04-15
PRIOR PLING DATE: 1997-04-15
PRIOR FILING DATE: 1997-04-15
PRIOR PILING DATE: 1997-04-15
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46.8%; Score 657.6; DB 3;
Best Local Similarity 76.4%; Pred. No. 1.8e-169;
Matches 836; Conservative 0; Mismatches 246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09981124 Patent No. US20020166144A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Crepis sp.
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Best Local Similarity 73.8%;
Matches 852; Conservative
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Publication No US20040168213A1

GENERAL INPORMATION:
APPLICANT: Verbeky, Michelle L.
APPLICANT: Baublite, Catherine
APPLICANT: Williams, Deryck J.
APPLICANT: Milliams, Deryck J.
APPLICANT: McLaird, Merry J.
APPLICANT: McLaird, Merry J.
APPLICANT: McLaird, Merry APPLICANTON: NUCLEIC ACIDS ENCODING ANTHELMINTIC
TITLE OF INVENTION: AGENTS AND PLANTS MADE THEREFROM
FILE REPRERENCE: 12057-016001
CURRENT APPLICATION NUMBER: US, 101772, 227
CURRENT FILING DATE: 2004-02-04
PRIOR FILING DATE: 2003-02-05
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 4.0
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; Publication No. US2005002270A1
; GENERAL INFORMATION:
APPLICANT: University of Kentucky Research Foundation
; APPLICANT: Hildebrand, David
APPLICANT: Hildebrand, David
; APPLICANT: HEADER TORNOKO
; TITLE OF INVENTION: RECOMBINANT STOKESIA EPOSYGENASE GENE
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                                                           TCTTGGGTGATTACAGGATGATCGACAGGACTCCATTTTTCAAAGCAATGTGGAGAGAGG
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Best Local Similarity 73.8%; Pred. No. 2.6e-166;
Matches 852; Conservative 0; Mismatches 290;
                                                                                                                                                                                                                                                         Sequence 12, Application US/10912534
Publication No. US20050172358A1
GENERAL INFORMATION:
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| NAME/KEY: CDS
| LOCATION: (1)...(1140)
| US-10-912-534-12
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APPLICANT: Green, Allan
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APPLICANT: Green, Allan
APPLICANT: Lenman, Marit
APPLICANT: Lenman, Marit
APPLICANT: Lenman, Marit
TITLE OF INVENTION: FATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES THEREFOR IN MODJ
TITLE OF INVENTION: FATTY ACID METABOLISM
TITLE OF INVENTION: FATTY ACID METABOLISM
TITLE OF INVENTION: PATTY ACID METABOLISM
TITLE OF INVENTION: PATTY ACID METABOLISM
CURRENT FILING DATE: 1090-04-10-17
PRIOR APPLICATION NUMBER: US 60/043706
PRIOR FILING DATE: 1997-04-15
PRIOR FILING DATE: 1997-04-15
PRIOR FILING DATE: 1997-04-15
PRIOR FILING DATE: 1997-04-15
PRIOR APPLICATION NUMBER: AU PO6226
PRIOR PILING DATE: 1997-04-15
PRIOR APPLICATION NUMBER: AU S 60/050403
PRIOR APPLICATION NUMBER: AU S 60/050403
PRIOR PILING DATE: 1997-04-15
PRIOR FILING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VERSION 3.1
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Pred. No. 1e-164;
0; Mismatches 256;
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09981124 Patent No. US20020166144A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                     CATAAAATGTAATC 1230
                                                                                                                                                                                                                                                                                                                         LENGTH: 1358
TYPE: DNA
ORGANISM: Crepis palaestina
FEATURE:
NAME/KEY: CDS
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Matches 826, Conservative
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COTHER INFORMATION
US-09-981-124-1
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                                                                                                                                                                                                                                            Score 640.4; DB 9;
Pred. No. 9.9e-165;
0; Mismatches 256;
               CURRENT APPLICATION NUMBER: US/10/622,774
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: 60/396,406
PRIOR FILING DATE: 2002-07-19
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.2
SEQ ID NO 10
                                                                                                                                                                                                                                            Query Match
Best Local Similarity 75.5%;
Matches 826; Conservative
                                                                                                                                                                     TYPE: DNA ORGANISM: Crepis palaestina
   FILE REFERENCE: 050229-0377
                                                                                                                                                 LENGTH: 1344
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APPLICANT: Kloek, Andrew P.
APPLICANT: Davila-Abonte, Jennifer A.
APPLICANT: Hresko, Michelle Coutu
APPLICANT: Hresko, Michelle Coutu
APPLICANT: Modaird, Merry B.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC
TITLE OF INVENTION: AGENTS AND PLANTS MADE THEREFROM
FILE REFERENCE: 12557-016001
CURRENT APPLICATION NUMBER: US/10/772,227
CURRENT APPLICATION NUMBER: US 60/445,293
PRIOR APPLICATION NUMBER: US 60/445,293
PRIOR FILING DATE: 2003-02-05
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 32
LENGTH: 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
45.4%; Score 638.6; DB 8;
Best Local Similarity 74.5%; Pred. No. 2.8e-164;
Matches 835; Conservative 0; Mismatches 274;
                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE: OTHER INFORMATION: hypothetical sequence
                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) NAME/KEY: CDS
; LOCATION: (1) ... (1122)
US-10-772-227-32
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                                TTGGGTGATTACAGGATGATCGACAGGACTCCATTTTTCAAAGCAATGTGGAGAGGACCC
          GTTTACTTAGCATGCCCGGTTTACTGGTTTTGCCAATCTTGCATCCTCACTGGTTTATGG
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US-10-772-227-32
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Sequence 32, Application US/10772227; Publication No. US20040168213A1; GENERAL INFORMATION: APPLICANT: Verbsky, Michelle L. APPLICANT: Baublite, Catherine; APPLICANT: Williams, Deryck J.

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1008 ACGITACACACCCCACGTGTTGCCATTGTTTCCCTACATTCTCACATTATCATGCA 1067
911 ATGITACACACACTCACGTCATGCATATGTTCTCATACATTCCACACTATCATGCTA 970
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                                                                                          948 TCAAAGGAGCCTTGACCACAATCGACAGATTTCGGTCTCCTGAATCGGGTTTTCCACG 1007
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Search completed: September 25, 2006, 00:33:09 Job time : 1702 secs

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Sequence 3

Sequence Sequence 13, Appl 13, Appl 15, Appl 17, Appl 17, Appl 15, Appl 17, Appl 15, Appl 15, Appl

Sequence

Scoring table:

Searched:

Minimum DB Maximum DB

Database

Perfect score:

Sequence:

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Run on:

Sequence Sequence Sequence Sequence Sequence

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Sequence

Sequence

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Sequence 3, Application US/08872302;
Patent No. 5846784
; GENERAL INFORMATION:
TITLE OF INVENTION: Fatty Acid Modifying Enzymes From
TITLE OF INVENTION: Developing Seeds of Vernonia galamenensis;
NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: P-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 870; DB 2; I
Pred. No. 2.3e-229;
US-08-320-982-44
US-08-819-037-44
US-09-045-940-44
US-08-675-650B-1
US-09-133-962A-3
US-09-133-962A-11
US-09-133-962A-11
US-09-134-028-028-11
US-09-354-231B-13
US-09-354-231B-15
US-09-354-231B-15
US-09-354-231B-17
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FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R
REGISTRATION NUMBER: P-41,173
REFERENCE/DOCKET NUMBER: BB-1084
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRONS: 302-773-0164
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86.1%;
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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    NAME/KEY:
LOCATION:
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1: /EWC Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
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8: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/PacMfiles1.seq:*
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Sequence 15,
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US-09-059-769-3
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US-09-161-962A-1
US-09-697-379-1
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US-09-697-379-15
US-09-697-379-15
US-09-697-379-15
US-09-697-379-15
US-09-697-379-15
US-09-185-578-1
US-08-314-596-43
US-08-314-596-43
US-08-314-596-39
US-08-314-596-39
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Maximum Match 100%
Listing first 45 summaries
                                                                         - nucleic search, using sw model
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Match Length
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Sequence 3, Application US/09059769
Patent No. 6129518
GENERAL INFORMATION:
APPLICANT: Green, Allan
APPLICANT: Lenman, Marit
APPLICANT: Lenman, Marit
APPLICANT: Singh, Surinder
APPLICANT: Strone, Sten
TITLE OF INVENTION: Plant Fatty Acid Epoxygenase Genes and Uses
TITLE OF SQUENCES: 20
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059,769
FILING DATE: April 14, 1998
PRICK APPLICATION NUMBER: US/09/059,769
FILING DATE: 15-APR-1997
PRICK APPLICATION NUMBER: US POC226
FILING DATE: 15-APR-1997
PRICK APPLICATION NUMBER: US 60/043706
FILING DATE: 16-APR-1997
PRICK APPLICATION NUMBER: US 60/043706
FILING DATE: 16-APR-1997
PRICK APPLICATION NUMBER: US 60/050403
ATTORING APPLICATION:
                                         1229 AAGGTGTATATTGGTACCATAAAATGTGATACGAGCTG 1266
             1200 AAGGGACATATTGGTACCATAAAATGTAATCGATGATG 1237
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                                                                                                                                                                                                                                                                                                      3: Greenlee, Winner and Sullivan, 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8089
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1312 base pairs
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Matches 836; Conservative
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STRANDEDNESS: single
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ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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LOCATION:
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                                                            149 ATGATCATAATATAAACGAACGTGCACCGGTTGATGCGGCACCATTCTCGTTAAGCGATC 208
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Patent No. 6129518
GENERAL INFORMATION:
APPLICANT: Green, Allan
APPLICANT: Lenman, Marit
APPLICANT: Lenman, Marit
APPLICANT: Stymne, Sten
TITLE OF INVENTION: Therefor
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12;
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/059,769

FILING DATE: April 14, 1998

PRIOR APPLICATION NUMBER: W P06223

FILING DATE: 15-APR-1997

PRIOR APPLICATION NUMBER: AU P06223

FILING DATE: 15-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU P06226

FILING DATE: 15-APR-1997
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Pred. No. 4.1e-166;
0; Mismatches 256;
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APPLICATION NUMBER: US 60/043706
FILING DATE: 16-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/050403
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (303) 499-8080
TELEPAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1358 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 75.5
Matches 826; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30..1151
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STATE: Colorado
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US-09-059-769-1
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RESULT 3
US-09-059-769-1
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                                                                                                                      ATTGCCTACATCTTCTTCCTTGCCAACACATATATCCCTAATCTCCCTCATCCTCTA 250
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                                                                                                                                                                                      GTCCTCGGCCATGAATGCGGCCATCATGCCTTTAGTGAGTACCAGTGGATTGATAACGCC 436
                                                                                                                                                                                                                                                                          311 ATCCTGGCCATGAATGTGGTCACCATGCCTATAGCAACTACACACTGGGTTGACGACACT 370
                                                                                                                                                                                                                                                                                                                                  GTTGGATTCGTCCTCCATTCGGCTCTCCCTCACCCCTTACTTTTCTTGGAAATACAGCCAT 496
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                                                                               CATAAAATGTAATC 1230
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Best Local Similarity 73.9
Matches 791; Conservative
                                                                                                                                                                                     TYPE: DNA
ORGANISM: Crepis alpina
                                                                                                                                                                                                                    NAME/KEY: CDS
; LOCATION: (1)..(1125)
US-09-161-994A-1
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Sequence 1, Application US/09161994A Patent No. 633448 GENERAL INFORMATION: APPLICANT: BAFOR, Maureen

RESULT 4 US-09-161-994A-1

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APPLICANT: BANAS, Antoni
APPLICANT: DAHLOVIST, Anders
APPLICANT: GUMMESON, Per-Olov
APPLICANT: GUMMESON, Per-Olov
APPLICANT: LEE, Michael
APPLICANT: STODAL, Staffan
APPLICANT: STONAE, Sten
APPLICANT: STYME, Sten
TITLE OF INVENTION: NOVEL PLANT ENZYME AND US
FILE REPRENCES: BAFOR=1
CURRENT APPLICATION NUMBER: US/09/161,994A
CURRENT FILING DATE: 1996-09-29
PRIOR FILING DATE: 1996-03-29
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                Score 426.2; DB 3;
Pred. No. 4.1e-107;
                                                                                                                                                                                                                                                                       0; Mismatches 448;
                                                                                                                                                                                                                                  30.3%; Score 426.2;
                                                     ORGANISM: Arabidopsis thaliana
IMMEDIATE SOURCE:
CLONE: p92103
                                                                                                                               NAME/KEY: CDS .
LOCATION: 93..1244
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                   Best Local Similarity 61.0%;
Matches 711; Conservative
  HYPOTHETICAL: NO
                  ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                             FEATURE
                                                                                                                                                                                               US-09-133-962A-1
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119 GCGCCGCCTGGGTGACGTGCATTTACGGAATTCCAGTTTTAGGCGTGTTTATTCT 778
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                                                                                                                                   GGAACTGGATCAAAGGAGCCTTGACCACAATCGACAGAGATTTCGGTCTCCTGAATCGGG 998
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                                                                                                                                                            GGAACTGGCTCAGAGGGGCTTTGTCAACAATCGATAGGGACTTTGGGTTCCTGAATAGTG
                                                         TCGTAATCACTTATCTGCACCACACACATCTGTCGTCACCCCATTACGATTCAACCGAAT
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JOHN JOSEPH OKULEY
TITLE OF INVENTION: GENES FOR MICROSOMAL FATTY ACID
DELTA-12 DESATURASES AND RELATED
ENZYMES FROM PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION UNDER: US/09/133,962A
FILING DATE: 14-Aug-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 07/977,339
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: CHRISTENBURY, LYNNE M.
REGISTRATION NUMBER: 30,971
REFERBUCE/DOCKET NUMBER: BB-1043-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302)992-5481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: UNITED STATES OF AMERICA ZIP: 19898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09133962A Patent No. 6372965
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1372 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (302)773-0164
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STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. D
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TITLE OF INVENTION: GENES FOR MICROSOMAL
PATTY ACID DELTA-12
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CORRESPONDENCE ADDRESS: 1. DU PONT DE NEMOURS
ADDRESSEE: E. I. DU PONT DE NEMOURS
AND COMPANY
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US-09-697-379-1
; Sequence 1, Application US/09697379
; Patent No. 6872872
; Patent No. GRANATION:
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US-09-763-331-5
i Sequence 5, Application US/09763331
j Patent No. 6625335
j GRNEAL INFORMATION:
i APPLICANT: Martin, Charles E.
APPLICANT: Mitchell, Andrew
ITILE OF INVENTION: Synthetic Fatty Acid Desaturase Gene for ITILE OF INVENTION: Synthetic Fatty Acid Desaturase Gene for ITILE REFERENCE: 97-0081 PCT 87-0081 PCT CURRENT APPLICATION NUMBER: US/09/763,331
CURRENT PILING DATE: 1999-08-24
PRIOR APPLICATION NUMBER: US 60/097,586
i PRIOR PILING DATE: 1998-08-24
i NUMBER OF SEQ ID NOS: 8
i PRIOR APPLICATION OF INTERPRETATION OF INTERPRETA
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APPLICANT: JOHATHAN EDWARD LICHTNER
JOHN JOSEPH OKULEY
WILLIAM DEAN HITZ
ANTHONY JOHN KINNEY
NARENDRA YADAV
LUIS PEREZ-GRAU
TITLE OF INVENTION: GENES FOR MICROSOMAL
PATTY ACID DELTA-12
DESATURASES AND
HYDROXYLASES FROM PLANTS
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NAME: Christenbury, Lynne M..
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB1043 US DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 992-5481
TELEFAX: (302) 892-1026
                                                                                                                                                                                                                   COMPUTER: MacIntosh
OPERATING SYSTEM: Microsoft Windows
SOFTWARE: Microsoft Word Version 7.
RENT APPLICATION DATA: BAPLICATION NUMBER: US/09/697,379
FILING DATE: 26-Oct-2000
CLASSIPICATION: <university of the control of the control
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APPLICATION NUMBER: U.S. 07/977,339
FILING DATE: 17-NOV-1992
APPLICATION NUMBER: U.S. 09/133,962
FILING DATE: 14-AUG-1998
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SEQUENCE DESCRIPTION: SEQ ID NO: 1:
STREET: 1007 MARKET STREET
                                                                                                                       ZIP: 19898
JTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                           CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
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Best Local Similarity
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US-09-133-962A-15
i Sequence 15. Application US/09133962A
; Patent No. 6372965
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: U.S. 09/697,379
FILING DATE: 26-0CT-2000
APPLICATION NUMBER: U.S. 09/133,962
FILING DATE: 14-AUG-1996
APPLICATION NUMBER: U.S. 08/262,401
FILING DATE: 20-UN-1994
APPLICATION NUMBER: U.S. 07/977,339
APPLICATION NUMBER: U.S. 07/977,339
FILING DATE: 15-0CT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: BB1043USDIV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 992-5481
                                                                                                                                                       ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYDE: Ploppy disk
COMPUTER: Dell
OPERATING SYSTEM: Windows 2000
SOFTWARE: Microsoft Word 97 SR-2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/116,212A
FILING DATE: 03-Apr-2002
CLASSIFICATION: «Unknown»
   NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS
AND COMPANY
STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Arabidopsis thaliana IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 93..1244
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Christenbury, Lynne M. REGISTRATION NUMBER: 30,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TYDECULE TYPE: cDNA
HYPOTHETICAL: NO
ANT-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (302) 892-1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                 CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                              545 ATTCCTAGAACTCAGTCCCAGCTCAGGACTTACTCCACATACGAATTTCTTGACAACG
                                                                                                                                                                                                                                                                                                                                                                                   CCTGGTCGAATCCTCATCTTGGTCATCATGTTAACCTTAGGATTTCCTTTATACCTCTTA
                                                                                                   ACTGGTTTATGGGTCCTCGGCCATGAATGCGGCCATCATGCCTTTAGTGAGTACCAGTGG
                                                                                                                                                                        ATTGATAACGCCGTTGGATTCGTCCTCCATTCGGCTCTCCTCACCCCTTACTTTTGG
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                                                                                                                                                                                                                                  COMPUTER READABLE FORM.
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATM:
APPLICATION NUMBER: US/09/133,962A
FILING DATE: 14-Augl1998
CLASSIFTCATION: cUrknown>
PRIOR APPLICATION DATA:
APPLICATION UNMBER: U.S. 07/977,339
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
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                  JOHN JOSEPH OKULEY

TITLE OF INVENTION: GENES FOR MICROSOMAL FATTY ACID
DELTA-12 DESATURASES AND RELATED
ENZYMES FROM PLANTS
                                                                                                                  ADDRESSE: T. DU PONT DE NEMOURS AND COMPANY STREET: 1007 MARKET STREET
CITY: WILLMINCTON
STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 30.2%; Score 424.6; DB 3; Best Local Similarity 60.9%; Pred. No. 1.6e-106; Matches 710; Conservative 0; Mismatches 449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: BB-1043-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 992-5481
TELEFAX: (302) 773-0164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: 521..1654
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-133-962A-15
   APPLICANT: JONATHAN EDWARD LIGHTNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: CHRISTENBURY, LYNNE M. REGISTRATION NUMBER: 30,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SECTION NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 2973 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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                                                                                 NUMBER OF SEQUENCES: 1/
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE · SOURCE
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GIGITGCACCATTIGITTCCCTACATTCCACATTATCATGCAAAGGAGGCAAGGCGAGGCC 1084
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US-10-116-212A-15
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30.2%; Score 424.6; DB 3; Length 2973;
Best Local Similarity 60.9%; Pred. No. 1.6e-106;
Matches 710; Conservative 0; Mismatches 449; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/697,379
FILING DATE: 26-0ct-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: U.S. 07/977,339
FILING DATE: 17-NOV-1992
APPLICATION NUMBER: U.S. 09/133,962
ATTORNEY/AGGAT: NRFORMATION:
REGISTRATION NUMBER: 30,971
REGISTRATION NUMBER: 30,971
REGISTRATION NUMBER: 30,971
TELEPAN: (302) 992-5481
TELEPAN: (302) 892-1026
                            OF INVENTION: GENES FOR MICROSOMAL
PATTY ACID DELTA-12
DESATURASES AND RELATED
ENZYMES FROM PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: Maccincom
OPERATING SYSTEM: Microsoft Windows 5
SOFTWARE: Microsoft Word Version 7.0
                                                                                                                                                                                                                                                                    ADDRESSEE: E. I. DU PONT DE NEMOURS
AND COMPANY
STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) SEQUENCE DESCRIPTION: SEQ ID NO: 15: US-09-697-379-15
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INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 2973 base_pairs
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STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                        CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
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                                                                                                                                                                                              NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
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ORIGINAL SOURCE:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                      .770 AAAGCAATCCCGCCGCATTGTTTCAAACGCTCAATCCCTCGCTCTTTCTCCTACCTTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTGGTTTATGGGTCCTCGGCCATGAATGCGGCCATCATGCCTTTAGTGAGTACCAGTGG
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                                                                                                                                                                                   125 CATGATATGGACGAACGAGCCCCGGATTGATCCGGCGCCCATTCTCGTTAAGTGATCTAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                    245 CAGGATCTCATTATCACCTTCCTTTTATACACGGTCGCCAACACCTACATTCCTCACCTC
                                                          TTCAGAAATCTGGGAGAAGGTAGCAGAATGTCGGATTCATATGATGATCGAATGAAGAT
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Indele
Mismatches 449;
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710; Conservative
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                                                                                                                  WILLIAM DEAN HITZ
ANTHONY JOHN KINNEY
NARENDA YADAU
LUIS PEREZ-GRAU
SPENEZ-GRAU
FINVENTION: GENES FOR MICROSOMAL
PATTY ACID DELTA-12
DESATURASES AND
HYDROXYLASES FROM PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 424.6; DB 3;
Pred. No. 1.6e-106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 09/697,379
FILING DATE: 26-0CT-2000
APPLICATION NUMBER: U.S. 09/133,962
FILING DATE: 14-AUG-1998
APPLICATION NUMBER: U.S. 08/262,401
FILING DATE: 20-UUN-1994
APPLICATION NUMBER: PCT/US93/09987
FILING DATE: 15-0CT-1993
APPLICATION NUMBER: U.S. 07/977,339
FILING DATE: 17-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Christenbury, Lynne M.
REGISTATION UNDRER: 30,971
REPRENCE/DOCKET NUMBER: BB1043USDIV2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: E. I. DU PONT DE NEMOURS
AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: Dell
OPERATING SYSTEM: Windows 2000
SOFTWARE: Microsoft Word 97 SR-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 521..1654
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-116-212A-15
                                                             APPLICANT: JONATHAN EDWARD LIGHTNER JOHN JOSEPH OKULEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (302) 992-548:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2973 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (302) 892-1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 835420
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   433..520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.2%;
60.9%;
                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLONE: pAGF2-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
Patent No. 6919466
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
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                                                                                                                                                                                                                                                 TITLE
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us-10-622-774-1.rni

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967 GAGAGGAGCTITAICAACIGTGGACAGAGAITAIGGGAITTIAAACAAGGITTITCCAIAA 1026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1069 GGAGGCAAGCGAGCCATCAAGCCAATCTTGGGTGATTACAGGATGATCGACAGGACTCC 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1129 ATTTTTCAAAGCAATGTGGAGAGAGGCCAAGGAATGCATTTACATCGAGCAAGATGCAGA 1188
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                                                              589 ATTICITGACAACACGCCTGGTCGAATCCTCATCTTGGTCATCATGTTAACCTTAGGATT 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    907 GTATTTGCAACACACTCACCTTTTGCCGCACTATGATTCCTCGGAGTGGGACTGGAT 966
553 AAGGGATGAAGTGTTCGTTCCCAAGAAAAATCTGGTTTAAGATGGTGGGCCAAACAC- 610
                                                                                                                                                                                                                                                           TGATCCATTGAGCCCGATCTTCACCGAGCGTGAGCGAATCCAGGTTGCGTTATCAGATCT 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    787 CGGCGTCCTCGCTGTCGCCTATGCGCTCTACCGTCTCGTGTTGGCCAAAGGGGTAGGTTG 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTGATGTGCATGTATGGAGTTCCAGTGATAGGTCTGAATTCCTTCATTATCGTAATCAC 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 847 Gerratradegritationegricearrariogrocitaacecerrerragiaargareae 906
                                                                                                                        ----trcaacaarccacccccccrrrcrcrcaarcaccarraccrraccrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracrracr
                                                                                                                                                                                                                                                                                                                                                                                              reaccerracececeararrrreceacececaaceacerecaarerararerereace
                                                                                                                                                                                                 TTATCTGCACCACACACATCTGTCGTCACCCCATTACGATTCAACCGAATGGAACTGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1189 CAGCAAGCACAAAGGGACATATTGGTACCATAAAATGTAATCGATGATGGAGTTT 1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1207 cgacaaggaraaaggrgrgrgrgrgrgrgragaaacaagcrrraaarartrgcarrr 1261
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Sequence 1. Application US/10185578

GENERAL INFORMATION:
APPLICANT: Shanklin. John
ITILE OF INVENTION: ISOform of Castor Oleate Hydroxylase
FILE REPREBNCE: DOW-07606
CURRENT APPLICATION NUMBER: US/10/185,578
CURRENT FILING DATE: 2002-06-28
PRIOR PILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 1.1
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; LOCATION: (1)..(1164)
; OTHER INFORMATION:
US-10-185-578-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 ATTITICIAATTIGGATTICAGAAAICIGGGAGAAGGIAGCAGAATGICGGATTCATATGA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arcrecarrrrandegreroganeardegreerdengendengrierdenrechaega 132
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                                                                                                                                                                                                                                                                                                                                                               | Sequence 5, Application US/09837751
| Patent NO. 6974898
| GENERAL INFORMATION:
| APPLICANT: Green, Allan
| APPLICANT: Green, Allan
| APPLICANT: Liu, Qing
| TITLE OF INVERTION: Method of Modifying the Content of Cottonseed Oil
| FILE REFERENCE: 45-00
| CURRENT APPLICATION NUMBER: US/09/837,751
| CURRENT PILING DATE: 2001-04-18
| PRIOR FILING DATE: 2000-04-18
| NUMBER OF SEQ ID NOS: 35
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Best Local Similarity 60.1%; Pred. No. 3.1e-105;
Matches 718; Conservative 0; Mismatches 471;
                                                                                                                                                                 1205 ACATATIGGTACCATAAAATGTAAT 1229
                                                                                                                                                                                                                                2784 GTGTACTGGTACAACAATAAGTTAT 2808
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SEQ ID NO 5
LENGTH: 1422
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) LOCATION: (98)..(1246)
US-09-837-751-5
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GENERAL INFORMATION:
APPLICANT: SOMERVILLE, CHRIS
APPLICANT: VAN DE LOO, FRANK
TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS
1091 AGGAGTGCTTGTTCGTCGAGCCAGATGAAGGAGCTCCTACACAAGGCGTTTTCTGGTACC 1150
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/314,596
FILING DATE: 26-SEP-1994
CLASSIFICATION: 41E
ATTORNEY/ACTOR
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62.1%; Pred. No. 1.2e-104;
iive 0; Mismatches 408;
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                                                                                                                                                                                              RESULT 14
US-08-314-596-43
; Sequence 43, Application US/08314596
; Patent No. 5668292
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ATTORNEY/AGENT INFORMATION:
NAME: ROKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 20690
TELECOMMUNICATION INFORMATION:
TELEPAX: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
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678; Conservative
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EDNESS: single
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CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN D
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COUNTRY:
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Matches 67
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                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/08/120,982
FILING DATE: 11-OCT-1994
CLASSIPICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29.7%; Score 417.2; DB 2; 62.1%; Pred. No. 1.2e-104; ive 0; Mismatches 408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSITICATION 1435

PRICASILICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/314,596
FILING DATE: 26-SEP-1994
ATTORNEY/AGBNT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 206905/1220
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 860.10 NO: 43:
SEQUENCE CHARACTERISTICS:
LINFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1222 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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Matches 678; Conservative
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TIGGATICGICCICCATICGGCICICCICACCCTIACTITICTIGGAAATACAGCCATC
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New isolated nucleic acid molecule encoding a delta 12-fatty acid epoxygenase enzyme, useful for genetically producing industrial products including coating, composites, adhesives and plasticizers.
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(HATA/) HATANAKA T.
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P-PSDB; ADW68587.
Stokesia laevis.
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expression; chimeric gene; recombinant enzyme; ss.
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                                                                 The present invention relates to a nucleic acid molecule encoding a delta 12-fatty acid epoxygenase enzyme. The invention is useful for genetically producting raw materials in the manufacture of industrial products including coating, composites, adhesives and plasticizers. The present sequence is the Stokesia laevis fatty acid epoxygenase cDNA.
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                                                                                                                                                                                                                                             Query Match
100.0%; Score 1406; DB 14; Length 1406;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1406; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                      Sequence 1406 BP; 403 A; 322 C; 289 G; 392 T; 0 U; 0 Other;
                         SEQ ID NO 1, 22pp; English
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The present invention relates to a nucleic acid molecule encoding a delta 12-fatty acid epoxygenase enzyme. The invention is useful for genetically producing raw materials in the manufacture of industrial products including coating, composites, adhesives and plasticizers. The present sequence is the Vernonia galamensis epoxygenase cDNA. Note: The present sequence is described as SEQ ID NO:9 in the sequence listing. But SEQ ID NO:11 on the page 2 of the specification.
                                                                                                                                                                                     AGGCCATCAAGCCAATCTTGGGTGATTACAGGATGATCGACAGGACTCCATTTTTCAAAG
                                                                                                                                                                                                       TGACTACAATCGATAGAGATTTCGGTCTCCTGAATAGGGTGTTCCATGACGTCACACAC
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epoxygenase enzyme, useful for genetically producing industrial
including coating, composites, adhesives and plasticizers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA purification; transgenic plant; plant; expression; seed oil; soybean oil; linseed oil; plastic; delta try acid epoxygenase; delta 12-epoxygenase; delta 12-epoxidase; de.
                                                                                                                                                                                                                                                                                                      AAGGGACATATTGGTACCATAAAATGTAATCGATGATG
                                                                                                                                                                                                                                                                                                                     Example 4; SEQ ID NO 9; 22pp; English
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                                                                                             The present sequence encodes Vernonia galamenensis fatty acid epoxidising enzyme. The present invention also describes: (1) Vernonia galamenensis fatty acid desaturase; (i1) chimeric genes comprising the fragments linked to regulatory sequences; and (iii) transformed host cells containing the chimeric genes. The DNA's from the present invention can be used to alter levels of expression of the enzymes in transformed host cells or to produce the recombinant enzymes by transformed host microbial host cells. (Updated on 27-AUG-2003 to correct OS field.)
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            DNA encoding Vernonia galamenensis fatty acid desaturase and fatty acid epoxidising enzyme - used to alter levels of expression of the enzymes transformed host cells or to produce recombinant enzymes.
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Pred. No. 5.9e-206;
0; Mismatches 155; Indels
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                                                                   Col 25-29; 21pp; English
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Best Local Similarity 86.1%;
Matches 963; Conservative (
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AEC02364 standard; cDNA; 1137
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ZENTELLA R.
WILLIAMS D J.
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                Length 1364;
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                Score 870; DB 14;
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Best Local Similarity 86.1%;
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The invention relates to a transgenic plant containing at least one DNA construct comprising: (a) a nucleic acid encoding a polypeptide effective for catalyzing the conversion of a substrate to a C16, C18, or C20 monounsaturated fatty acid product; and (b) a regulatory element operably linked to the nucleic acid encoding the polypeptide and conferring expression in a vegetative tissue of the plant. Also described: (1) a method of making a transgenic plant; (2) an isolated nucleic acid comprising the nucleotide sequence; (3) a recombinant nucleic acid comprising the nucleotide sequence; (3) a recombinant nucleic acid construct comprising at least one regulatory element that confers expression in a vegetative tissue of a plant; and (4) a method of screening a transgenic plant for anthelmintic activity. The transgenic plant is useful in preparing compounds having anthelmintic activity. The present sequence encodes an epoxygenase which is used in the exemplification of the present invention.
C16,
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Williams DJ;
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ADR87346 standard; cDNA; 1134
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                                                                                                                                 GACCCTGCTCCTTTTTCTCTTTTCTGATCTTAAGAAGGCTATTCCAGCTCATTGCTTTAGA 120
                                                                                                                                                     AGATCTGCTGTTTGGTCTTCTTGCTATGTGGTGCAAGACCTTATTATTACTTTTCTTTTG 180
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                                                                                                                                                                                                                                             CCGGTTTACTGGTTTTGCCAATCTTGCATCCTCACTGGTTTATGGGTCCTCGGCCATGAA 391
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                                                                AACAGAGIGITCCATGACGIGACTCATACTCATGIGCTTCATCATCTTTTCCCATATATT
                                            Gaps
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                      Length 1137;
Sequence 1137 BP; 288 A; 228 C; 219 G; 402 T; 0 U; 0 Other;
                                            Indels
                      Score 697; DB 14;
Pred. No. 5.8e-163;
                                           275;
                                           0; Mismatches
                    49.6%;
ilarity 75.8%;
Conservative
                               Similarity
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The present invention relates to transgenic plants (I) containing one or more DNA constructs have a nucleic acid encoding a protein effective for catalyzing the conversion of a substrate to a 16C, 18C or 20C monounsaturated fatty acid product, e.g. a fatty acid cooxygenase or a fatty hydroxylase, and a regulatory element operably linked to the nucleic acid encoding the protein, where the regulatory element confers expression in vegetative tissue of the plant. The fatty caid epoxygenase or a fatty hydroxylase can be confersion acid acid proxygenase or a fatty hydroxylase can be confersion acid and epoxy-fatty acid, e.g., vernolic acid, e.g., ricinoleic acid and epoxy-fatty acid, e.g., vernolic acid, in cay expetative tissue. The DNA construct of (I) is useful in the production of hydroxylases and epoxygenases that controls nematode damage in commercially important plant species and so (I) is wibbits increased commercially important plant species and so (I) in exhibits increased commercially important plant species and so (I) in exhibits increased commercially important plant species and so (I) in exhibits increased commercially individue nematode metabolism, growth, viability, development, infectivity and/or the nematode life cycle. (I) provides
ATGATCGACAGGACTCCATTTTTCAAAGCAATGTGGAGAGAGGCCAAGGAATGCATTTAC 1171
                                                               1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18C monounsaturated fatty acid, 20C monounsaturated fatty acid; fatty acid expression fatty acid; proxygenae; fatty hydroxylase; phospholipid; diacylglycerol; acyltransferae; pDAT; diacylglycerol; acyltransferae; pDAT; histoleic acid; epoxy-fatty acid; vernolic acid; hydroxy-fatty acid; ricinoleic acid; epoxy-fatty acid; vernolic acid;
                                                                                                                                                                                                                                                                                          1081 ATTGAACAAGATGCTGACTCTAAGGCATAAGGGAACTTATTGGTATCATAAGATGTAA 1137
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monounsaturated fatty acid product, useful for controlling nematodes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nematocide; Plant; 16C monounsaturated fatty acid;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydroxylase/ epoxygenase coding sequence, SEQ ID
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Zentella R;
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ACAGGACTCCATTTTTCAAAGCAATGTGGAGAGGCCAAGGAATGCATTTACATCGAGC 1178
965 ATCATGCAAAGGAGGCAAGAGATGCAATCAAACCAGTTTTGGGTGATTATTATAAGATTG 1024
                                 1179 AAGATGCAGACAGCAAGCACAAAGGGACATATTGGTACCATAAAATGTAA 1228
                                                                                                                                                                                                              Stokesia laevis epoxygenase encoding cDNA
                                                                                                                                                                                                                                                                                                      /*tag= a
/product= "epoxygenase"
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Williams D
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KLOEK A P.
DAVILA-APONTE J
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Zentella
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WILLIAMS D J.
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P-PSDB; AEC02269.
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MCLAIRD M B.
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Mclaird MB,
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(HRES/)
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                                                                                                  Gaps
  season-long nematode control, thus providing labor savings, by recthe need for and frequency of chemical control. The present sequent the coding sequence for one such fatty acid epoxygenase and fatty hydroxylase used to ilustrate the invention.
                                                                             Score 681.6; DB 13; Length 1134;
Pred. No. 3.9e-159;
0; Mismatches 229; Indels 6;
                                                        Sequence 1134 BP; 297 A; 268 C; 229 G; 340 T; 0 U; 0 Other;
                                                                             48.5%;
                                                                                         Best Local Similarity 78.0
Matches 835; Conservative
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The invention relates to a transgenic plant containing at least one DNA construct comprising: (a) a nucleic acid encoding a polypeptide effective for catalyzing the conversion of a substrate to a cl6, Cl8, or C20 monounsaturated fatty acid product; and (b) a regulatory element operably linked to the nucleic acid encoding the polypeptide and conferring expression in a vegetative tissue of the plant. Also described: (1) a method of making a transgenic plant; (2) an isolated nucleic acid comprising the nucleotide sequence; (3) a recombinant nucleic acid construct comprising at least one regulatory element that confers expression in a vegetative tissue of a plant; and (4) a method of screening a transgenic plant for anthelmintic activity. The present sequence encodes an epoxygenase which is used in the
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                                                                                   DB 14; Length 1134;
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                                           Sequence 1134 BP; 297 A; 268 C; 229 G; 340 T; 0 U; 0 Other;
                                                                               Query Match 48.5%; Score 681.6; DB 14; Length Best Local Similarity 78.0%; Pred. No. 3.9e-159; Matches 835; Conservative 0; Mismatches 229; Indels
exemplification of the present invention.
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This invention describes a novel isolated nucleic acid sequence (I)
encoding a Calendula officinalis calendulic acid desaturase polypeptide.
CC free invention also describes (I) a process for producing unsaturated
fatty acids, comprising introducing at least one copy of (I) or (II) into
an oil-producing organism, growing the organism, isolating oil from the
CC organism and releasing fatty acids from the oil, (2) a process for
producing triglycerides with an increased unsaturated fatty acid content,
CC producing organism, growing the organism and isolating oil from the
CC producing organism, growing the organism, isolating oil from the organism, (3) a process for producing saturated fatty acids, comprising
introducing organism, growing the organism, isolating oil from the organism, and releasing fatty acids from the oril; (4) a process for producing
CC triglycerides with an increased saturated fatty acid content, comprising
CC triglycerides with an increased saturated fatty acid content, comprising
CC triglycerides with an increased saturated fatty acid content, comprising
CC triglycerides with an increased saturated fatty acid content.
CC producing organism, growing the organism and isolating oil from the
CC organism; (5) an enzyme capable of converting a diunsaturated fatty acid
CC of to a triunsaturated fatty acid. Transgenic organism; (specially plants) containing one or more copies of (I) are useful for producing
CC organisms (especially plants) containing one or more norientated fatty
CC organisms (especially plants) containing one or more organisms content.
CC organisms (especially plants) containing one or more organisms (especially
CC organisms (especially plants) containing one or more organisms (especially
CC organisms (especially plants) containing one or more organisms
CC organisms (especially plants) containing one or more organisms
CC organisms (especially for producing oils with an increased saturated fatty
CC denomic sequences by homology screening. This sequence encodes the
1025 ATAGGACTCCGATATTCAAAGCAATGTGGAGAGAGAGGGCCAAGGAATGCATCTATATCGAGC 1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid sequence encoding Calendula officinalis calendulic acid desaturase, useful for e.g. producing transgenic plants having oil with an increased unsaturated fatty acid content,.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Calendula; calendulic acid desaturase; unsaturated fatty acid; oil;
triglyceride; transgenic plant; ds.
                                                                                                                                                              1179 AAGATGCAGACAGCAAGCACAAAGGGACATATTGGTACCATAAAATGTAA 1228
                                                                                                                                                                                                                                1085 CAGATGAAGATACTGAACACAAGGGTGTTTACTGGTACCATAAAATGTGA 1134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C. officinalis calendulic acid desaturase encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "calendulic acid desaturase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fritsche K, Peitzsch N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF88311 standard; DNA; 1285 BP
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The present invention relates to transgenic plants (I) containing one or more DNA constructs. The DNA constructs have a nucleic acid encoding a protein effective for catalyzing the conversion of a substrate to a 16C, 18C or 20C monounsaturated fatty acid product, e.g. a fatty acid encoding the conversion of a substrate to a 16C, 18C or 20C monounsaturated fatty acid product, e.g. a fatty acid epoxygenase or a fatty hydroxylase, and a regulatory element operably clement confers expression in vegetative tissue of the plant. The fatty clement confers expression in vegetative tissue of the plant. The fatty caid epoxygenase or a fatty hydroxylase can be phospholipididacylglycerol acyltransferase (DAGAT). (I) has an increased amount of hydroxy-fatty acid, e.g., ricinoleic acid and epoxy-fatty acid, e.g., vernolic acid, in a cycletative tissue. The DNA construct of (I) is useful in the production of hydroxylases and epoxygenases that controls nematode damage in commercially important plant species and so (I) exhibits increased controls infective, environmentally safe methods of inhibiting nematode metabolism, growth, viability, methods of inhibiting nematode metabolism, growth, viability, educing season-long nematode control, thus providing labor savings, by reducing
ACAGGACTCCAATTTTCAAAGCAATGTATAGAGAGGGCTAAGGAATGCATCTACATCGAGC 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                              Nematocide, Plant, 16C monounsaturated fatty acid,
18C monounsaturated fatty acid, 20C monounsaturated fatty acid,
fatty acid epoxygenase, fatty hydroxylase; phospholipid:diacylglycerol,
acyltransferase, PDAT, diacylglycerol, acyltransferase, DAGAT,
hydroxy-fatty acid, ricinoleic acid, epoxy-fatty acid, vernolic acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel transgenic plant containing DNA construct having nucleic acid encoding polypeptide for catalyzing conversion of substrate to monounsaturated fatty acid product, useful for controlling nematodes.
                                                                                                               1126 CCGATGAGGATAGCGAGCACAAAGGTGTGTTCTGGTACCACAAGATGTAATCAAAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. .1134
*tag= a
/product= "Codon optimised Hydroxylase/ epoxygenase"
                                                                              1179 AAGATGCAGCAAGCACAAAGGCACATATTGGTACCATAAAATGTAATGGATGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Davila-Aponte JA;
                                                                                                                                                                                                                                                                                                                                                                                                   Codon optimised hydroxylase/ epoxygenase coding sequence, SEQ ID 33
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Zentella R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 74; SEQ ID NO 33; 180pp; English.
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Mclaird MB,
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                                                                                                                                                          Gaps
            calendulic acid desaturase described in the method of the invention
                                                                                                            Length 1285;
                                                          Sequence 1285 BP; 364 A; 294 C; 253 G; 374 T; 0 U; 0 Other;
                                                                                                                                                          Indels
                                                                                                       Query Match

47.9%; Score 673; DB 4; L
Best Local Similarity 77.2%; Pred. No. 5.6e-157;
Matches 833; Conservative 0; Mismatches 240;
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Location/Qualifiers
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DAVILA-APONTE J A
HRESKO M C.
MCLAIRD M B.
ZENTELLA R.
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the need for and frequency of chemical control. The present sequence is the coding sequence for one such fatty acid epoxygenase and fatty hydroxylase, which has been codon optimised for improved plant expression.
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965 ATCATGCAAAGGAGGCAAGAGATGCAATCAAACCAGTTTTGGGTGATTATTATAAGATTG 1024
                                                                                                                                      New transgenic plant having a DNA construct comprising a nucleic acid encoding a protein for catalyzing the conversion of a substrate to a CIS or C20 monounsaturated fatty acid product, useful in preparing anthelmintic compounds.
                                                                                   ACAGGACTCCATTTTTCAAAGCAATGTGGAGGAGGCCCAAGGAATGCATTTACATCGAGC
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                                                                                                                                                                                                                                                               1179 AAGATGCAGACCAAGCACACAAAGGGACATATTGGTACCATAAAATGTAA 1228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transgenic plant; anthelmintic; epoxygenase; gene;
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The present invention relates to transgenic plants (I) containing one or more DNA constructs have a nucleic acid encoding a protein effective for catalyzing the conversion of a substrate to a 16C, protein effective for catalyzing the conversion of a substrate to a 16C, 18C or 20C monounsaturated fatty acid product, e.g. a fatty acid epoxygenase or a fatty hydroxylase, and a regulatory element operably linked to the nucleic acid encoding the protein, where the regulatory clement confers expression in vegetative tissue of the plant. The fatty acid epoxygenase or a fatty hydroxylase can be phospholipid:diacylglycerol acyltransferase (PDAT) or diacylglycerol acyltransferase (PDAT) or diacylglycerol acyltransferase (PDAT) or diacylglycerol acyltransferase (PDAT) (I) has an increased amount of hydroxylaty, acid, e.g., vernolic acid, in a vegetative tissue. The DNA construct of (I) is useful in the production a vegetative tissue. The DNA construct of (I) is useful in the production commercially important plant species and so (I) exhibits increased resistance to nematodes. (I) provides an effective, environmentally safe methods of inhibiting nematode metabolism, growth, viability, each of the present sequence is the need for and frequency of chemical control. The present sequence is
ATAGGACTCCTATATTCAAAGCAATGTGGAGAGAGGGCCAAGGAATGCATCTATATGGAGC 1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18C monounsaturated fatty acid, 20C monounsaturated fatty acid, fatty acid epoxygenase, fatty hydroxylase; phospholipid:dlacylglycerol, acyltransferase; PDAT; dlacylglycerol; acyltransferase; DAGAT, hydroxy-fatty acid; ricinoleic acid; epoxy-fatty acid; vernolic acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel transgenic plant containing DNA construct having nucleic acid encoding polypeptide for catalyzing conversion of substrate to monounsaturated fatty acid product, useful for controlling nematodes.
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                                                                            AAGATGCAGACAGCAAGCACAAAGGGACATATTGGTACCATAAAATGTAA 1228
                                                                                                                   1085 CAGATGAAGATACTGAACACAAGGGTGTTTACTGGTACCATAAAATGTAA 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "Hydroxylase/ epoxygenase"
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Zentella R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nematocide; Plant; 16C monounsaturated fatty acid;
                                                                                                                                                                                                                                                                                                                                                                                                            Hydroxylase/ epoxygenase coding sequence, SEQ ID
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Mclaird MB,
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Pred. No. 3.8e-155;
0; Mismatches 239; Indels 6;
                                                       Sequence 1134 BP; 299 A; 259 C; 225 G; 351 T; 0 U; 0 Other;
       exemplification of the present invention.
                                                                                                         47.38;
                                                                                                                                                          Conservative
                                                                                                                                   Similarity
                                                                                                                                Best Local Simi
Matches 825;
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DAVILA-APONTE J A
HRESKO M C.
MCLAIRD M B.
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the coding sequence for one such fatty acid epoxygenase and fatty hydroxylase used to illustrate the invention.
                                                                                Score 657.8; DB 13; Length 1125;
Pred. No. 3.3e-153;
0; Mismatches 262; Indels 12;
                                                 Sequence 1125 BP; 285 A; 277 C; 234 G; 329 T; 0 U; 0 Other;
                                                                                 Query Match
Best Local Similarity 75.6%;
Matches 847; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C16,
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CATITITCAAAGCAATGTGGAGAGGCCAAGGAATGCATTTACATCGAGCAAGATGCAG
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Williams DJ;
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This cDNA clone, designated CrepX, codes for a novel epoxygenase (see AAW19743) of a Crepis sp. (not Crepis palaestina) that has a high termolic acid content. The CrepX gene shows a high degree of homology to the novel Cpala delta-12-epoxygenase gene (see AAV63101) of C. alaestina. CrepX cDNA was isolated from a Crepis sp. cDNA library using a Crepis alpina acetylenase partial gene sequence (see AAV63104) as probe. The invention relates generally to novel genetic sequences (see AAV63104) as probe. The invention relates generally to novel genetic sequences (see AAV63104) as provide the means by which fatty acid metabolism can be manibulated in e.g. yeast, mould, bacteria, insects, birds, mammals and plants

( especially oilseed plants such as flax), in particular to convert unsaturated fatty acids to epoxygenated fatty acids. The invention extends to genetically modified oil-accumulating organisms and to the
              AGGAGGCAAGCGAGGCCATCAAGCCAATCTTGGGTGATTACAGGATGATCGACAGGACTC 1127
                                       971 AAGAGGCAAGGAATGCAATACAATCATAGGCGACTATTATATGATCGATAGGACTC 1030
                                                                         CATITITICAAAGCAAIGIGGAGAGAGGCCAAGGAAIGCAITIACAICGAGCAAGAIGCAG 1187
                                                                                            Fatty acid epoxygenase; CrepX; delta-12-epoxygenase;
mixed function monooxygenase; epoxygenated fatty acid; transgenic plant;
vegetable oil; oilseed; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated fatty acid epoxygenase gene - used particularly for transforming plants for producing modified oils for use in, e.g. coatings, resins, glues, plastics, surfactants or lubricants.
                                                                                                                                                      1085 ATAGCAAGCGCAAAGGTGTGTATTGGTACCATAAATTGTGA 1125
                                                                                                                                     ACAGCAAGCACAAAGGGACATATTGGTACCATAAAATGTAA 1228
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plant is useful in preparing compounds having anthelmintic activity. The present sequence encodes an epoxygenase which is used in the exemplification of the present invention.
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                                                                                                                                                                                                                                   TTAGTGAGTACCAGTGGATTGATAACGCCGTTGGATTCGTCCTCCATTCGGCTCTCCTCA
                                                                                                                        Gaps
                                                                                                                        12;
                                                                                       Query Match
46.8%; Score 657.8; DB 14; Length 1125;
Best Local Similarity 75.6%; Pred. No. 3.3e-153;
Matches 847; Conservative 0; Mismatches 262; Indels 12;
                                                            Sequence 1125 BP; 285 A; 277 C; 234 G; 329 T; 0 U; 0 Other;
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Arabidopsis thaliana.
Synthetic.
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 used in production of
                                                                 12;
                                              DB 2; Length 1312;
                            BP; 347 A; 301 C; 263 G; 399 T; 0 U; 2 Other;
                                                                 Indels
          resins, glues, plastics, surfactants or lubricants
                                              Score 657.6; DB 2;
Pred. No. 3.8e-153;
0; Mismatches 246;
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 These
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Best Local Similarity 76.4%;
Matches 836; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nematocide; Plant; 16C monounsaturated fatty acid; 18C monounsaturated fatty acid; 20C monounsaturated fatty acid; 20C monounsaturated fatty acid; 20C monounsaturated fatty acid epoxygenaes, fatty hydroxylase; phospholipid:diacylglycerol; acyltransferase; DAGT; diacylglycerol; acyltransferase; DAGT; hydroxy-fatty acid; ricinoleic acid; epoxy-fatty acid; vernolic acid; nematode; gene; ss; FAD2.
TIGGGCGACTITIATATGATCGATAGGACTCCAATTITAAAAGCAATGTGGGGGGGGC
                                                                                                            Novel transgenic plant containing DNA construct having nucleic acid encoding polypeptide for catalyzing conversion of substrate to monounsaturated fatty acid product, useful for controlling nematodes.
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Location/Qualifiers
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of hydroxylases and epoxygenases that controls nematode damage in commercially important plant species and so (1) exhibits increased resistance to nematodes. (1) provides an effective, environmentally safe methods of inhibiting nematode metabolism, growth, viability, development, infectivity and/or the nematode life cycle. (1) provides season-long nematode control, thus providing labor savings, by reducing the need for and frequency of chemical control. The present sequence is hydroxylase used to illustrate the invention. The encoded protein is a fusion protein where the N-terminal sequence of the epoxygenase and fatty.
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TGCTAGGCGTATTTACCCTTTTCGATATCATCACGTACTTGCACCACCACCATCAGTCGT
                                                                                                 CICCICATIAIGACICAACIGAAIGGAACIGGAICAAGAGGGGCGIIGICAGCAAICGAIA
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                                                      CACCCCATTACGATTCAACCGAATGGAACTGGATCAAAGGAGCCTTGACCACAATCGACA
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Williams DJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid molecule encoding a delta 12-fatty acid epoxygenase enzyme, useful for genetically producing industrial products including coating, composites, adhesives and plasticizers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACGIGAGCGGTITICAGGICTITICGGATCTIGGCCTICTIGCTGTGTTTATGGAA 715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGGAGAAAGGTAGCAGAATGTCGGATTCATATGATGATCGAATGAAAGATCATGATATGG 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                            invention relates to a transgenic plant containing at least one DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                Length 1143;
                                                                                                                                                                                                                                                                                                                                           Sequence 1143 BP; 291 A; 279 C; 243 G; 330 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 290; Indels
                                                                                                                                                                                                                                                                                                                                                                              Score 646; DB 14;
Pred. No. 2.8e-150;
                                                                                                                                                                                                                                                                                                        exemplification of the present invention.
                         NO 12; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 73.8%;
Matches 852; Conservative
                         SEQ ID
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including coating, composites, adhesives and plasticizers. The present sequence is the Crepis palaestina epoxygenase cDNA. Note: The present sequence is described as SEQ ID NO:10 in the sequence listing. But SEQ NO:12 on the page 2 of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGGITITIGATITATCATGTTCACCCTAGGATTTCCTTTATACCTCTTGACAAATATTTCC
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                                                                                                                                                             12; Gaps
                                                                        Query Match
Best Local Similarity 75.5%; Pred. No. 7.3e-149;
Matches 826; Conservative 0; Mismatches 256; Indels 12;
                                                      Sequence 1344 BP; 344 A; 308 C; 278 G; 414 T; 0 U; 0 Other;
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Db 969 TTGTTTTCATACATTCCACACTATCATGCAAGGGGTGCAATCAAGCCAATC 1028

Qy 1097 TTGGGTGATTACAGGATGATCGACAGGACTCCATTTTTCAAGGCATGTGGAGAGAGGC 1156

Db 1029 TTGGGCGACTTTTATATGATCGACAGGACTCCAATTTTAAAGCAATGTGGAGAGGCC 1186

Qy 1157 AAGGAATGCATTTACATCGACGAGACAGCAAGCACAAAGGGACATGTGGTAC 1216

Db 1089 AGGGAGTGCATTACATCGAGCAGACAGCACAAAGGGACATATGGTAC 1216

Qy 1217 CATAAAATGTAATC 1230

Qy 1217 CATAAAATGTAATC 1230

Db 1143 CATAAAATGTAATC 1156
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completed: September 25, 2006, le : 1366 secs

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3460, Ap
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/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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/EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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US-10-912-534-38
US-10-912-534-36
US-10-912-534-42
US-10-912-534-42
US-10-912-534-41
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 GenCore version (c) 1993 - 2006
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28	1279	61.3	383	ß	US-10-732-923-4737	Sequence 4737,	7, Ap
53	1271	6.09	383	m	US-09-981-124-12	Sequence 12,	12, Appl
30	1271	6.09	383	Ŋ	US-10-732-923-4789	Sequence 4789	9, Ap
31	1268.5	8.09	379	Ŋ	US-10-732-923-4888	Sequence 4888	8, Ap
32	1265	9.09	387	'n	US-10-732-923-4871	Sequence 4871	1, Ap
33	1264	9.09	383	Ŋ	US-10-732-923-4956	Sequence 4956	6, Ap
34	1263	60.5	383	4	US-10-424-599-266787	Sequence 26678	787,
35	1263	60.5	383	S	US-10-732-923-4910	Sequence 4910	0, Ap
36	1263	60.5	383	Ŋ	US-10-732-923-4911	Sequence 4911	1, Ap
37	1263	60.5	392	4	US-10-425-114-56017	Sequence 56017	17, A
38	1263	60.5	395	4	US-10-425-114-40643	Sequence 40643	43, A
39	1260	60.4	382	Ŋ	US-10-732-923-4755	Sequence 4755	5, Ap
40	1259	60.4	383	ß	US-10-732-923-4909	Sequence 4909	9, Ap
41	1258	60.3	383	4	US-10-772-227-128	Sequence 128,	, App
42	1258	60.3	383	ഗ	US-10-732-923-4930	Sequence 4930	0, Ap
43	1258	60.3	383	Ŋ	US-10-912-534-128	Sequence 128	, App
44	1255.5	60.2	382	ß	US-10-732-923-4882	Sequence 4882	2, Ap
45	1255	60.2	387	ഗ	US-10-732-923-4872	Sequence 4872	2, Ap

## ALIGNMENTS

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                                                         APPLICANT: University of Kentucky Research Foundation
APPLICANT: Hildebrand, David
APPLICANT: Hildebrand, David
APPLICANT: Hildebrand, David
APPLICANT: Hildebrand, David
TITLE OF INVENTION: RECOMBINANT STOKESIA EPOSYGENASE GENE
FILE REFERENCE: 050229-0377
CURRENT APPLICATION NUMBER: US/10/622,774
CURRENT PILING DATE: 2003-07-21
PRIOR PILING DATE: 2002-07-19
PRIOR FILING DATE: 2002-07-19
NUMBER OF SEQ ID NOS: 10
SOTWARE: Patentin version 3.2
SEQ ID NO 2
Sequence 2, Application US/10622774 Publication No. US20050022270A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 378; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Stokesia laevis
US-10-622-774-2
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Query Match
Best Local Similarity 72.0*
Matches 272; Conservative
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; ORGANISM: Stokesia laevis
US-10-772-227-36
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                                                                                                                                                                     APPLICANT: Werbsky, Michelle L.
APPLICANT: Baublite, Catherine
APPLICANT: Baublite, Catherine
APPLICANT: Rick, Andrew P.
APPLICANT: Klesk, Michelle Coutu
APPLICANT: Hresko, Michelle Coutu
APPLICANT: Hresko, Michelle Coutu
APPLICANT: Hresko, Michelle Coutu
APPLICANT: Milliams, Deryck J.
APPLICANT: Williams, Deryck J.
APPLICANT: Williams, Deryck J.
TILLE OF INVENTION: WUCKERC ACIDS ENCODING ANTHELMINTIC AGENTS AND
TILLE OF INVENTION: PLANTS MADE THEREFROM
FILE REFERENCE: 12557-02301,
CURRENT APPLICATION NUMBER: US,10/912,534
CURRENT PILING DATE: 2004-08-04
PRIOR FILING DATE: 2004-02-04
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Pred. No. 1.3e-196;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 140
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 136
                                                                                                                        // Sequence 136, Application US/10912534
// Publication No. US20050172358A1
// GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 36, Application US/10772227; Publication No. US20040168213A1; GENERAL INFORMATION:
APPLICANT: Verbsky, Michelle L.; APPLICANT: Baublite, Catherine
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361 IEQDADSKHKGTYWYHKM 378
                  361 IEODADSKHKGTYWYHKM 378
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US-10-912-534-136
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Best Local Similarity 99.5
Matches 376, Conservative
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61 YTVANTYIPHLPPPLVYLAWPVYWFCQSCILITGLWVLGHECGHHAFSEYQWIDNAVGFVL 120
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APPLICANT: Williams, Deryck J.
APPLICANT: Kloek, Andrew P.
APPLICANT: Loavila-Abonte, Jennifer A.
APPLICANT: Hresko, Michelle Coutu
APPLICANT: Hresko, Michelle Coutu
APPLICANT: McLaird, Merry B.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING THEREROM
FILE REFERENCE: 12557-016001
CURRENT PELING: 12557-016001
CURRENT FILING DATE: 2004-02-04
PRIOR APPLICATION NUMBER: US 60/445,293
PRIOR APPLICATION NUMBER: US 60/445,293
PRIOR APPLICATION NUMBER: US 60/445,293
PRIOR SEQ ID NOS: 130
SOFTWARE: FRACEEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 377
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APPLICANT: Baublite, Catherine
APPLICANT: Baublite, Catherine
APPLICANT: Williams, Deryck J.
APPLICANT: Milliams, Deryck J.
APPLICANT: Milliams, Deryck J.
APPLICANT: Milliams, Deryck J.
APPLICANT: McLaira, McLelle Coutu
APPLICANT: McLaira, Merry B.
TITLE OF INVENTION: MUCLEIC ACIDS ENCODING ANTHELMINTIC
TITLE OF INVENTION: AGENTS AND PLANTS MADE THEREFROM
FILE REFERENCE: 12557-016001
CURRENT PELLING DATE: 2004-02-04
PRIOR PILLING DATE: 2004-02-04
PRIOR PLILING DATE: 2003-02-05
PRIOR PLILING DATE: 2003-02-05
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181 MLTLGFPLYLLTNVSGKKYDRFTNHFDPLSPIFTERERIQVALSDLGIVAVFYGLKFLVQ 240
                                                                                                                                                            300 NRVFHDVTHTHVLHHLISYIPHYHAKBARDAIKPVLGDYYKIDRTPIFKAMWREAKECIY 359
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                                                                    62 FFLATTYITVLPAPLAYIAWFVYWFCQASILTGLWVIGHECGHHAFSEYQWIDDTVGFIL
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                                              61 YTVANTYIPHLPPPLVYLAWPVYWFCQSCILTGLWVLGHECGHHAFSEYQWIDNAVGFVL
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7 MSDLSDGK----NLLKRVPVDP-PFTLSDIKKAIPPHCFKRSVIRSSYYVVHDLIVSYVF
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APPLICANT: Verbaky, Michelle L.
APPLICANT: Baublite, Catherine
APPLICANT: Baublite, Catherine
APPLICANT: Baublite, Catherine
APPLICANT: Michek, Michelle Coutu
APPLICANT: Hresko, Michelle Coutu
APPLICANT: Michalzd, Merry B.
APPLICANT: Williams, Deryck J.
APPLICANT: WILLIANG MADE THEREFROM
FILE REFERENCE: 12557-023001
CURRENT APPLICATION NUMBER: US/10/912,534
CURRENT APPLICATION NUMBER: US 10/772,227
PRIOR FILLING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 140
SOFTWARE: PastSEQ for Windows Version 4.0
SOFTWARE: PastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 36, Application US/10912534 Publication No. US20050172358A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360 IEPDEDTEHKGVYWYHKM 377
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CRGANISM: Stokesia laevis
US-10-912-534-36
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US-10-772-227-42

Sequence 42, Application US/1077227

Publication No. US20040168213A1

GENERAL INFORMATION:
APPLICANT: Bublite, Catherine
APPLICANT: Milliams, Deryck J.
APPLICANT: McLark Marry B.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC
TITLE OF INVENTION: AGENTS AND PLANTS MADE THEREFROM
FILE REPRENCE: 12557-016001

CURRENT APPLICATION NUMBER: US/10/772,227

CURRENT APPLICATION NUMBER: US 60/445,293

PRIOR PLLING DATE: 2003-02-05

NUMBER OF SEQ ID NOS: 130

SOFTWARE: PARKSEQ for Windows Version 4.0
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74.3%; Score 1549.5; DB 4
Best Local Similarity 72.0%; Pred. No. 2.2e-144;
Matches 272; Conservative 47; Mismatches 52;
  SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 38 LENGTH: 377
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US-10-772-227-42
                                                                                             ; ORGANISM: Stokesia laevis
US-10-772-227-38
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Best Local Similarity
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LENGTH: 377
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                                                                                                                                                                                        APPLICANT: Verbaky, Michelle L.
APPLICANT: Baublite, Catherine
APPLICANT: Baublite, Catherine
APPLICANT: Baublite, Catherine
APPLICANT: Michek, Michelle Coutu
APPLICANT: Hresko, Michelle Coutu
APPLICANT: Hresko, Michelle Coutu
APPLICANT: Milliams, Deryck J.
TITLE OF INVENTION: WOUCLEIC ACIDS ENCODING ANTHELMINTIC AGENTS AND
TITLE OF INVENTION: PLANTS MADE THEREFROM
FILE REFERENCE: 12557-023001
CURRENT FILING DATE: 2004-08-04
PRIOR APPLICATION NUMBER: US 10/772,227
FRIOR FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 140
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 42:
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Publication No. US20050108791A1
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
FILE REFERENCE: 38-15 (52796) C
CURRENT APPLICATION NUMBER: US/10/732,923
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                                                                                                                    Sequence 42, Application US/10912534
Publication No. US20050172358A1
GENERAL INFORMATION:
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ORGANISM: Stokesia laevis
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US-10-732-923-4878
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  180 RLTLGPPLYLLTNISGKKYQRPANHFDPLSPIFTERERIQVLVSDLGLLAVIYAIKLLVA 239
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APPLICANT: Baublite, Cacherine
APPLICANT: Rlock, Andrew P.
APPLICANT: Klock, Andrew P.
APPLICANT: Klock, Michelle Coutu
APPLICANT: Hresko, Michelle Coutu
APPLICANT: McLaird, Merry B.
APPLICANT: Williams, Desyck J.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC AGENTS AND TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC AGENTS AND TITLE OF INVENTION: NUMBER: US/10/912,534
CURRENT PILING DATE: 2004-08-04
FRIOR APPLICATION NUMBER: US 10/772,227
FRIOR FILING DATE: 2004-02-04
NUMBER OF SEQ ID NOS: 140
SOPTWARE: FREESEQ for Windows Version 4.0
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9 Sequence 38, Application US/10912534

9 Publication No. US20050172358A1
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61 YTVANTYIPHLPPPLVYLAWPVYWFCQSCILTGLWVLGHECGHHAFSEYQWIDNAVGFVL 120
                                                                                                                                                                                                MLTLGFPLYLLTNVSGKKYDRFTNHFDPLSPIFTERERIQVALSDLGIVAVFYGLKFLVQ 240
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                                                                                                                     HSALLTPYFSWKYSHRKHHANTNSLENEEVYIPRTQSQLRTYSTYEFLDNTPGRILILVI
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GENERAL IN CORTATION:
GENERAL IN CORTATION:
APPLICANT: Baublite, Catherine
APPLICANT: Baublite, Catherine
APPLICANT: Baublite, Catherine
APPLICANT: Mary B.
APPLICANT: Midlaid, Merry B.
APPLICANT: Williams, Deryck J.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC AGENTS AND
TITLE OF INVENTION: PLANTS
TITLE OF INVENTION: DEANTS
TITLE OF INVENTION: UNCERC ACIDS SOURCE
CURRENT APPLICATION NUMBER: US/10/912,534
CURRENT FILING DATE: 2004-08-04
FILE REFERENCE: 1255-0230H
FILE REFERENCE: 2004-02-04
FILE REFERENCE: 2004-03-04
FILE REFERENCE: 2004-02-04
FILE REFERENCE: 2004-03-04
FILE R
                               Gaps
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                               63; Indels
69.0%; Pred. No. 6.9e-140; tive 50; Mismatches 63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 41, Application US/10912534 Publication No. US20050172358A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                               261; Conservative
      Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 LLTPYFSWKYSHRKHHANTNSLENEEVYIPRTQSQLRTYSTYEFLDNTPGRILILVIMLT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 LLTPYFSWKYSHRNHHANTNSLDNDEVYIPKRKSKVKIYS--KLLNNPPGRVFTLVFRLT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGFPLYLLTNVSGKKYDRFTNHFDPLSPIFTERERIQVALSDLGIVAVFYGLKFLVQTKG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 IGFPLYLLTNISGKKYGRFANHFDPMSPIFNDRERVQVLLSDFGLLAVFYAIKLLVAAKG 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 FGWVMCMYGVPVIGLNSFIIVITYLHHTHLSSPHYDSTEWNWIKGALTTIDRDFGLLNRV 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 AAWVINMYAIPVIGVSVPFVLITYLHHTHLSLPHYDSTEWNWIKGALSTIDRDFGFLNRV 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         303 FHDVTHTHVLHHLLSYIPHYHAKBARDAIKPVLGEYXKIDRTPIFKAMYREAKECIYIEP 362
                                                                                                                                                                                                                                                                                                                                                                                                                   8 RMKD----HDMDERAPIDPAPFSLSDLKKAIPAHCFRRSAVWSSCYVVQDLIITFLLYTV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64
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                                                                                                                                                                                                                                                                                                   DB 5; Length 377;
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APPLICANT: Baublite, Catherine
APPLICANT: Baublite, Catherine
APPLICANT: Williams, Deryck J.
APPLICANT: Kloek, Andrew P.
APPLICANT: Kloek, Andrew P.
APPLICANT: McLarid, Mcrip B.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC
TITLE OF INVENTION: AGENTS AND PLANTS MADE THEREFROM
FILE REFERENCE: 12557-016001
CURRENT FILLING DATE: 2004-02-04
PRIOR PLILING DATE: 2004-02-05
PRIOR PLILING DATE: 2003-02-05
NUMBER OF CONTINUED BELLING DATE: 2003-02-05
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                                                                                                                                                                                                                                                                                                73.0%; Score 1523.5; DB 5
71.7%; Pred. No. 8.2e-142;
tive 45; Mismatches 54;
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SOGTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 41
IENGTH: 374
TYPE: PRT
ORGANISM: Artificial Sequence
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   CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: 10/310,154
PRIOR FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 24149
SEQ ID NO 4878
LENGTH: 377
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Publication No. US20040168213A1
GENERAL INFORMATION:
                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Calendula officinalis
US-10-732-923-4878
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DEDSEHKGVFWYHKM 377
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Best Local Similarity
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255
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                                                                                           GKKYDRFANHFDPMSPIFKERERFQVFLSDLGLLAVFYGIKVAVANKGAAWVACMYGVPV
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                                                                                                                                                                                                                                                                                                                                    316 LPPYIPHYHAKEASEAIKPILGDYRMIDRTPFFKAMWREAKECIYIEQDADSKHKGTYWY
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                                                                    RICHHANTINSLENEEVYI PRIQSQLRTYSTYEFLDNTPGRILILVIMLTLGFPLYLLTNVS
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Baublite, Catherine
APPLICANT: Baublite, Catherine
APPLICANT: Macrew P.
APPLICANT: Hresko, Michelle Coutu
APPLICANT: Hresko, Michelle Coutu
APPLICANT: Michalrd, Merry B.
APPLICANT: Williams, Deryck J.
TITLE OF INVENTION: DUCLEIC ACIDS ENCODING ANTHELMINTIC AGENTS AND
TITLE OF INVENTION: PLANTS MADE THEREFROM
FILE REFERENCE: 12557-023001
CURRENT APPLICATION NUMBER: US 10/772,227
FRIOR APPLICATION NUMBER: 108 10/772,227
FRIOR FILING DATE: 2004-08-04
NUMBER OF SEQ ID NOS: 140
SOFTHARE FEASTER OF WINDOWS VERSION 4.0
SOFTHARE: PASTERG for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 137, Application US/10912534; Publication No. US20050172358A1; GENERAL INFORMATION:
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Matches 260; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Crepis biennis
US-10-912-534-137
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APPLICANT: Green, Allan
APPLICANT: Green, Allan
APPLICANT: Green, Allan
APPLICANT: Green, Marit
APPLICANT: Green, Marit
APPLICANT: Stymme, Stem
ITILE OF INVENTION: FATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES THEREFOR IN MOD
TITLE OF INVENTION: FATTY ACID METABOLISM
FILLS REFERENCE: 26-98 ATTY ACID METABOLISM
FILLS REFERENCE: 26-98 ATTY ACID METABOLISM
FILLS REFERENCE: 2001-10-17
PRIOR APPLICATION NUMBER: US 60/043706
PRIOR PILING DATE: 1997-04-16
PRIOR FILING DATE: 1997-04-16
PRIOR PELING DATE: 1997-04-15
PRIOR PELING DATE: 1997-06-20
                                                                                                                                                                                                                                                                                         NRVFHDVTHTHVLHHLFPYIPHYHAKEASEAIKPILGDYRMIDRTPFFKAMWREAKECIY 360
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                                                  240
                                                                                                                                                                                                    241 TKGFGWVMCMYGVPVIGLNSFIIVITYLHHTHLSSPHYDSTEWNWIKGALTTIDRDFGLL 300
                                                                                                                                                                                                                             239 KKGAAWVACMYGVPMLGVFTLFDIITYLHHTHQSSPHYDSTEWNWIRGALSAIDRDFGFM 298
                                                                                                                                                                                                                                                                                                                  299 NSVFHDVTHTHVMHHMPSYIPHYHAKEARDAINTIIGDYYMIDRTPILKALWREAKECMY 358
                                                                                                                                                           179 MPTLGFPLYLLINISGKKYDRFANHFDPMSPIFKERERFQVLLSDLGLLAVFYGIKVAVA 238
                             HSALLTPYFSWKYSHRKHHANTNSLENEEVYIPRTQSQLRTYSTYEFLDNTPGRILLILVI 180
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                                                                                                                MITLGFPLYLLTNVSGKKYDRFINHFDPLSPIFTERERIQVALSDLGIVAVFYGLKFLVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRATURE:
NAME/KEY: misc feature
LOCATION: (1927). (1927)
OTHER INFORMATION: The 'Xaa' at location 292 stands for Arg, or Ser.
NAME/KEY: misc feature
LOCATION: (9377). (937)
OTHER INFORMATION: N is any nucleotide residue
LOCATION: (9017). (901)
COTHER INFORMATION: N is any nucleotide residue
COTHER INFORMATION: N is any nucleotide residue
US-09-981-124-4
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12.0%; Score 1501; DB 3; Length 373;
Best Local Similarity 71.3%; Pred. No. 1.4e-139;
Matches 259; Conservative 48; Mismatches 52; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       314 MFSYIPHYHAKEARDAINTIIGDYYMIDRTPILKALWREAKECMYIE--PDSKRKGVYWY 371
239 KKGAAWVACMYGVPMLGVFTLFDIITYLHHTHQSSPHYDSTEWNWIRGALSAIDRDFGFM 298
                                                     NRVFHDVTHTHVLHHLFPYIPHYHAKEASEAIKPILGDYRMIDRTPFFKAMWREAKECIY 360
                                                                        299 NSVFHDVTHTHVWHHMPSYIPHYHAKEARDAINTIIGDYYMIDRTPILKALWREAKECMY 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 VYLAMPVYWFCQSCILTGLWVLGHECGHHAFSEYQWIDNAVGFVLHSALLTPYFSWKYSH 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 RKHHANTNSLENEEVYIPRTQSQLRTYSTYEPLDNTPGRILILVIMLTLGFPLYLLTNVS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKKYDRFTNHFDPLSPIFTERERIQVALSDLGIVAVFYGLKFLVQTKGFGWVMCMYGVPV 255
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                                                                                                                                                                                                                                                                                               APPLICANT: Verbally,
APPLICANT: Verballe, Catherine
APPLICANT: Williams, Deryck J.
APPLICANT: Williams, Deryck J.
APPLICANT: Williams, Deryck J.
APPLICANT: Moder, Andrew P.
APPLICANT: Hresko, Michelle Coutu
APPLICANT: McLaird, Merry B.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING ANTHELMINTIC
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: AGENTS AND PLANTS MADE THEREFROM
FILER REPREBRICE: 12557-016001
CURRENT FILING DATE: 2004-02-04
PRIOR APPLICATION NUMBER: US 60/445,293
PRIOR APPLICATION NUMBER: US 60/445,293
PRIOR PLING DATE: 2003-02-05
NUMBER OF SEQ 1D NOS: 130
SOFTWARE: FASESQ for Windows Version 4.0
                                                                                                                                                                                                                                                Sequence 18, Application US/10772227
Publication No. US20040168213A1
GENERAL INFORMATION:
                                                                                                                          361 IEQDADSKHKGTYWYHKM 378
                                                                                                                                                359 IE--PDSKRKGVYWYHKL 374
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Best Local Similarity 71.19
Matches 258; Conservative
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ORGANISM: Crepis biennis
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RESULT 15

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76 VYLAWPVYWFCQSCILTGLWVLGHECGHHAFSEYQWIDNAVGFVLHSALLTPYFSWKYSH 135
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                                                GENERAL INFORMATION: VO. USZUGOSII/2339A1

APPLICANT: VETDEKY, Michelle L.
APPLICANT: Baublite, Catherine
APPLICANT: Baublite, Andrew P.
APPLICANT: Baublite, Andrew P.
APPLICANT: Davila-Aponte, Jennifer A.
APPLICANT: McLaird, Merry B.
APPLICANT: Actella, Rodolfo
APPLICANT: Alliams, Deryck J.
TITLE OF INVENTION: PLANTE AND THEREFROM
FILE REFERENCE: 1257-023001
CURRENT APPLICATION NUMBER: US/10/912,534
CURRENT APPLICATION NUMBER: US/10/712,227
PRIOR APPLICATION NUMBER: US 10/772,227
PRIOR APPLICATION NUMBER: US 10/772,227
PRIOR APPLICATION NUMBER: US 10/772,227
SOFTWARE: PSECSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.8%; Score 1498; DB 5;
71.1%; Pred. No. 2.7e-139;
iive 48; Mismatches 53;
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Sequence 18, Application US/10912534
Publication No. US20050172358A1
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Matches 258; Conservative
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ORGANISM: Crepis biennis
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AF1882631 Vernonia
AF28534 Vernoria
AF785537 Locus cor
AF22534 Vernicia
AF774324 Borago of
AC166091 Clycine m
AL071892 Prunus ar
AF771844 Helianthu
AF251844 Helianthu
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AJ879071 AB188252

AY525163 C DQ157776 J AF188264 V

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AY803000 AY803001 AY803002 AY803003

AY803004

AY802998

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ALIGNMENTS

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AY802998 I AY802999 I

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Stokesia laevis delta 12 fatty acid epoxygenase mRNA, complete cds.
AY462108
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Stokesia laevis

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterida; campanulida; Asterales; Asteraceae; Cichorioideae;
Vernonieae; Stokesia.

1 (bases i to 1406)

Hatanaka, T. and Hildebrand, D.F.

Expression of a Stokesia laevis Epoxygenase Gene
Unpublished.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 1406)
Hatanaka T. and Hildebrand, D.F.
Direct Submission
Submitted (10-NOV-2003) Plant Resource Science, Kobe University,
1-1 Rokkodai, Nada, Kobe, Hyogo 657-8501, Japan
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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VERSION
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SOURCE
ORGANISM
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JOURNAL
REFERENCE
AUTHORS
TITLE
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AUTHORS
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Y16283 Crepis pala
CS023933 Sequence
CS023943 Sequence
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                 GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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QVILSDFGLLAVFYJIKLLVAAKGAAKONYINNYA PVLGVSVFPVLITYLHTHLSLPH
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Fritsche, K., Hornung, E., Peitzsch, N., Renz, A. and Feussner, I. Isolation and characterization of a calendic acid producing (8,11)-linoleoyl desaturase
FEBS Lett. 462 (3), 249-253 (1999)
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/protein_id="CAB64256.1"
/db_xref="G1:6634080"
/db_xref="G0A:098CG2"
/db_xref="UniProtKB/TrEMBI:Q98CG2"
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/organism="Calendula officinalis'
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Fatty acid deseturase gene from plants
Patent: WO 0116362-A 1 08-MAR-2001;
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1312 bp DNA linear PAT 27-AUG-2002
Plant fatty acid epoxygenase genes and uses therefor.
BD061165.
BD061165.1 GI:22606771
JP 2001518797-A/2.
Crepis sp.
Crepis sp.
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
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289 CCCCGTGGGCTTACTTAGCATGGCCGGTTTACTGGTTTTGTCAAGCTAGCATCCTCACTG
                                                529 CTAAACGCAAGGCCAAAGTTGCAGTTTACTCAA-----AGCTTCTTAACAATCCCCTG
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                                                                                              ATAACGCCGTTGGATTCGTCCTCCATTCGGCTCTCCTCACCCTTACTTTCTTGGAAAT
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IRSSYYVVHDLIVAYVFYFLANTYIPLLPTPWAYLAWPVYWFCQASILTGLWVIGHEC
GHHAYSDYQLIDDIVGFVLHSALYTPYFSWKYSHRNHHANTNSLDNDEVYIPKRKAKV
ACAGGACTCCATTTTTCAAAGCAATGTGGAGAGAGGCCAAGGAATGCATTTACATCGAGC 1178
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YVYLSDIGILAVLYATKLLIVEBKGAANTCKYLL I VLGYHRFYLLTYLHTHLSLDH
YDSTEWNWI RIGALST I DRDFGFLIRVFHDVITHYLLHL I SY I PHYHAKEARDA I KPV
LGEFYKI DRTPI FKAMMREAKECI Y I EPDEDSEHKGTYWYHKM"
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                                                                                                               1179 AAGATGCAGACAGCAAGCACAAAGGGAACATATTGGTACCATAAAATGTAATCGATGATG 1237
                                                                                                                                                1184
                                                                                                                                                                                                                                                                                                                                                Helianthus annuus Streptophyta; Embryophyta; Tracheophyta; Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Core eudicotyledons; Spermatophyta; Magnoliophyta; eudicotyledons; care eudicotyledons; asterids; campanulids; Asterales; Asteraceae; Asteroideae;
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                                                                                                                                                                                                                                  AY166773 1419 bp mRNA linear PLN 02-JUN-?
Helianthus annuus deltal2-fatty acid acetylenase mRNA, complete
                                                                    ACATCCTCGAACGTGTCCCCATTGATC---CACCATTCACTCTAAGTGATCTAAAGAAAG
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1 (bases 1 to 1419)
Cahoon, E.B., Schnurr, J.A., Huffman, E.A. and Minto, R.E. Fungal responsive fatty acid acetylenases occur widely evolutionarily distant plant families
Plant J. 34 (5), 671-683 (2003)
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protein id="AAO38032.1"
/db_xref="GI:31322135"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cahoon, B.B.
Direct Submission
Submitted (18-OCT-2002) Crop Genetics, DuPont, Blu
Experimental Station, Wilmington, DE 19880-0402, Location/Qualifiers
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Pred. No. 4.1e-150;
0; Mismatches 252;
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/organism="Helianthus annuus"
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/db_xref="taxon:4232"
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                                                                                                                                                                                                                                                         CCCCATTACGATTCAACCGAATGGAACTGGATCAAAGGAGCCTTGACCACAATCGACAGA 976
                                                                                                                                                                                                                                                                                    1 (bases 1 to 1312)
Green, A., Singh, S., Lenman, M. and Stymne, S.
Plant fatty acid epoxygenase genes and uses therefor
Patent: US 6329518-A 3 11-DEC-2001,
BASF Plant Science GmbH and Commonwealth Scientific & Industrial
Research Organisation; Ludwigshafen;
DEX;
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                                                                        AAGTTTCTTGTACAAACAAAAGGATTTGGTTGGGTGATGTGCATGTATGGAGTTCCAGTG
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Sequence 3 from patent US 6329518.
AR367438
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/organism="unknown"
/mol_type="mRNA"
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Matches 836; Conservative
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; asterids; campanulids; Asterales; Asteraceae; Cichorioideae; Cichorioaea; Cropis.

1 (bases 1 to 1312)
Stymne, S., Green, A., Singh, S. and Lenman, M.
Plant fatty acid epoxygenase genes and uses therefor Patent: JP 201518797-A 2 16-007-2001;
COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION, STEN
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PN JP 2001518797-A/2

PD 16-071-2001

PF 05-APR-1998 JP 1998543302

PR 15-APR-1997 AU

16-APR-1997 US 60/043706,20-UN-1997 US 60/050403 PI

STYMNE,ALLAN GREN, SURINDER SINGH, MARIT LENMAN PC

C12N15/53,C12N9/02

CC Strandedness: Single;

CC Topology: Linear;

FH Key

26. 1147.
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    /organism="Crepis sp."
    /mol_type="genomic DNA"
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asterids, campanulids, Asterales, Asteraceae, Cichorioideae,
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GREEN ALLAN (AU); SINGH SURINDER (AU); COMM (AU); STYMNE STEN (SE); LENMAN MARIT (SE)

Location/Qualifiers
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Best Local S:
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; endicotyledons; core eudicotyledons;

Spermatophyta; Magnoliophyta; endicotyledons; core eudicotyledons;

asterids; campanulids; Asterales; Asteroideae;

Calenduleae; Dimorphotheca.

El (bases 1 to 979)

Cahoon, E.B., Schnurr, J.A., Huffman, E.A. and Minto, R.E.

Fungal responsive fatty acid acetylenases occur widely in evolutionarily distant plant families

L plant J. 34 (5), 671-683 (2003)

El Cahoon, E.B.

Direct Submission

Direct Submission
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Experimental Station, Wilmington, DE 19880-0402,
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
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Patent: WO 2005014831-A 3 17-FEB-2005;
The University of York (GB)
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                                             895 GCAATCATACCAGTTTTGGGTGAATTTTATAAGATCGATAGGACTCCAATCTTTAAAGCA
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PD 16-OCT-20001
PP 09-APR-1998 JP 1998543302
PR 15-APR-1997 AU PO 6223,15-APR-1997 AU PO 6226 P
R 15-APR-1997 US 60/043706,20-JUN-1997 US 60/050403 PI S
STYMME, ALLANG OREEN, SURINDER SINGH, MARIT LENMAN PC
C12N15/53,C12N9/02
CC Strandedness: Single;
CC Topology: Linear;
FH Key 30. 1151.
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JP 2001518797-A/1.
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Pred. No. 3.4e-144;
0; Mismatches 256;
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/db_xref="taxon:4577"
                                                                                      1142 ATGTGGAGAGGCCAAGGAATGC 1165
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Location/Qualifiers
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/organism="Zea mays"
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Best Local Similarity 75.5%;
Matches 826; Conservative
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
asterids, campanulids, Asterales, Asteraceae, Cichorioideae,
Cichorieae, Crepis.
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Pred. No. 3.4e-144;
0; Mismatches 256;
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/organism="Crepis palaestina"
/mol type="unassigned DNA"
/db_xref="taxon:72611"
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Patent: WO 2005014833-A 3 17-FEB-2005;
The University of York (GB)
Location/Qualifiers
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Pred. No. 3.4e-144;
0; Mismatches 256;
              1. 1358
/organism="Crepis palaestina"
/mol_type="unassigned DNA"
/db_xref="taxon:72611"
 Location/Qualifiers
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Query Match 45.5%; Score 640.4; DB 2; Length 1358; Best Local Similarity 75.5%; Pred. No. 3.4e-144; Matches 826; Conservative 0; Mismatches 256; Indels 12; Gaps 2;	Qy 137 GAACGAGCCCGATTGATCCGGCGCCATTCTCGTTAAGTGATCTAAAGAAAG	Oy         197 GCACATTGCTTCCGGCGATCCGCCGTCTGGTCATCTACGTAGTTCAGGATCTCATT         256           nh         135 CCCCATTGCTTCAGGATCTACGTTCATCTAGTTCAGGATCTTCATT         194	257 ATCACCTTCCTTTTATACACGGTGGCCAACACCTACATTCCTCACCTCCTCCTCTCTCT	317 GTTACTTAGCATGGCCGGTTTACTGGTTTTGCCAATCTTGCATCCTCACTGGTTTATGG 316 GTTACTTAGCATGGCTTTACTGGTTTTGCCAATCTTGCATCTTGCAAGCTTATGG 317 GTTACTTAGCAGCTTTACTGGTTCTGTCAAGCTAGGCTTATGG	377 GTCCTCGGCCATCATGCGCCATCATGCCTTTAGTGAGTACCAGTGGATTGATAACGCCCCTTTAGTGAGTACCAGTGGATTGATAACGCCCCCCCC	437 GTTGGATTCGTCCTTTCGCTCTCCTCACCCCTTACTTTTCTTGGAAATACAGCCAT 375 GTTGGATTCGTCTTCTCTCTCTCTCTCCTCTTACTTTTCTTTGGAAATTCACCATCAC	497 CGAAAGCACCATCCAAAATTCACTCGAAAACGAGGAGTTTACATTCCTAGAACT 435 CGGAATCACCATTCCAAACAAGTTCGATTGATAACGATGAAGTTTTACATTTCCGAAAAGC	557 CAGTCCCAGCTCAGGACTTACTCCACATTTCTTGACAACACGCCTGGTCGAATC	617 CTCATCTTGGTCATCATGTTAACCTTAGGATTTCCTTTATACCTCTTAACGAATGTTCA	677 GGCAAGAAGTACGATAGATTTACCAACTTTGATCCATTGAGCCGGATCTTCACCGAG	737	Oy 797 AAGTITCITGIACAAACAAAGGAITIGGIIGGGGGAIGIGCAIGIAIGGAGIICCAGIG 856	Db 789 TIAGGCGTATTIACCTTTTTCGATGATCACCTTCTTGCACCACACCA			606	ч	115		Qy 1157 AAGGAATGCATTTACATCGAGCAAGATGCAGACAGCAAAGGGACATATTGGTAC 1216
	Qy 617 CTCATCTTGGTCATGTTAACCTTAGGATTTCCTTTATACCTTTAACGAATGTTTCA 676  bb 549 TTGGTTTTGATTATCATGTTCACCCTAGGATTTCCTTTATACCTCTTGACAATATTTCC 608	Oy 677 GGCAAGAAGTACGATAAGATTTACCAACCACTTGATCCATTGAGCCCGATCTTCACCGAG 736	Oy 737 CGTGAGCGAATCCAGGTTATCAGATCTTGGTATCGTTGCAGTGTTTACGGACTC 796	QY 797 AAGTTTCTTGTACAAAGGATTTGGTTGGTAGGGATGGGATGGAGTTCCAGTG 856	QY 857 ATAGGTCTGAATTGCTTATCGTAATCACTTATCTGCACCACACACA	OY 917 CCCCATTACGATTGAACGGAACTGGATCAAAGGAGCCTTGACCACAATCGACAG 976	QY 977 GATTTCGGTCTCCTGAATCGGGTTTTCCACGACGTTACACACAC	OY 1037 TIGITICCCTACATTACCACATACCAAAGGAGGCAAGCGAGGCCATCAAGCCAATC 1096	Oy 1097 TTGGGTGATTACAGGATGATCGACACCCATTTTTCAAAGCAATGTGGAGAGGGGC 1156	OY 1157 AAGGAATGGATTACATCGAGCAAGACCAGCAAGCAACAGCAAAGGGACATATTGGTAC 1216	Oy 1217 CATAAATGTAATC 1230  Db 1143 CATAAATTGTGATC 1156	RESULT 13 CS023971 LOCUS LOCUS CS023971 1358 bp DNA linear PAT 03-MAR-2005 DEFINITION Sequence 5 from Patent WO2005014834.		Lrepis palaestina NISM Crepis palaestina Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tri	Spermatophyta; Magnollophyta; eudicotyledons; core eudicotyledons; asterids; campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae; Crepis.	REFERENCE 1 AUTHORS REAL, A. TITULE PARTY SOLID MICHAGIA 3	JOURNAL Patent: WO 2005014834-A 5 17-FEB-2005; The University of York (GB)	FEATURES Location/Qualifiers 1. 1358   Arcaniem="Granie nalaestina"	/mol_type="unassigned DNA" /db_xref="taxon:72611"	ORIGIN

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/ COUGUI 2011 1 d = "CACO9644.1"

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DSTEMNMIRGALSAIDRDFGFLMSVFHDVFHTHVMHHLESYIPHYHAKEARDAIKPIL
GDFYMIDRTFLLKAMMREGRECMYIEPDSKLKGVYMYHKL"
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                                    CGTGAGCGAATCCAGGTTGCGTTATCAGATCTTGGTATCGTTGCAGTGTTTTACGGACTC
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GREEN ALLAN (AU) ; SINGH SURINDER (AU) ; COMMW SCIENT (AU) ; STYNNE STEN (SE) LENMAN MARIT (SE)
LOCATION/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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Green, A., Singh, S., Lemman, M. and Stymne, S.
Plant fatty acid epoxygenase genes and uses therefor
Patent: US 6329518-A 1 11-DEC-2001,
BASF Plant Science GmbH and Commonwealth Scientific & Industrial
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DEX;
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    1358
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  AR367437.1 GI:34600636
                                                              CATAAATGTAATC 1230
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1143 CATAAATTGTGATC 1156
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Best Local Similarity 75.5
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  Length 1358;
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Query Match 45.5%; Score 640.4; DB 2; Best Local Similarity 75.5%; Pred. No. 3.4e-144; Matches 826; Conservative 0; Mismatches 256;
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